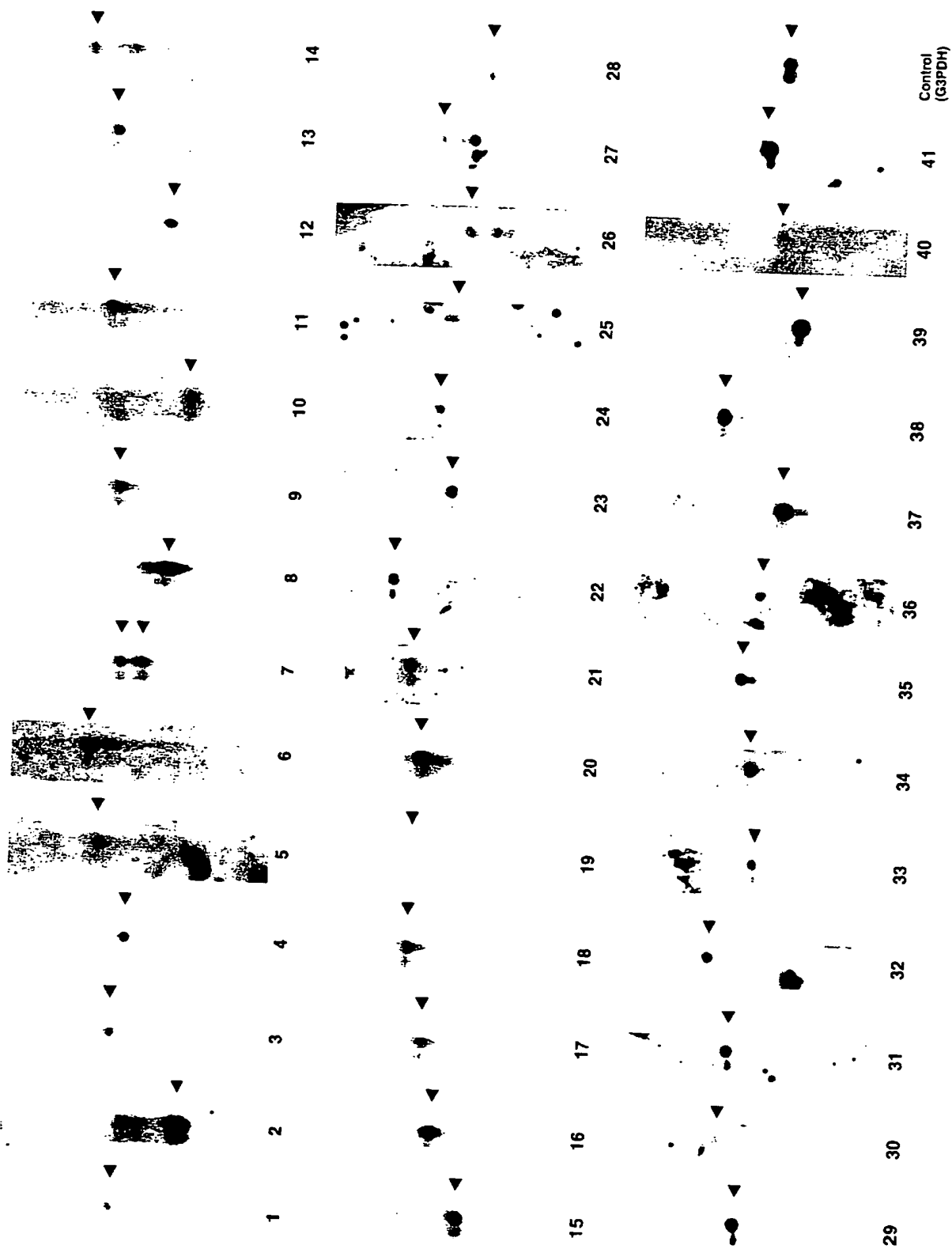
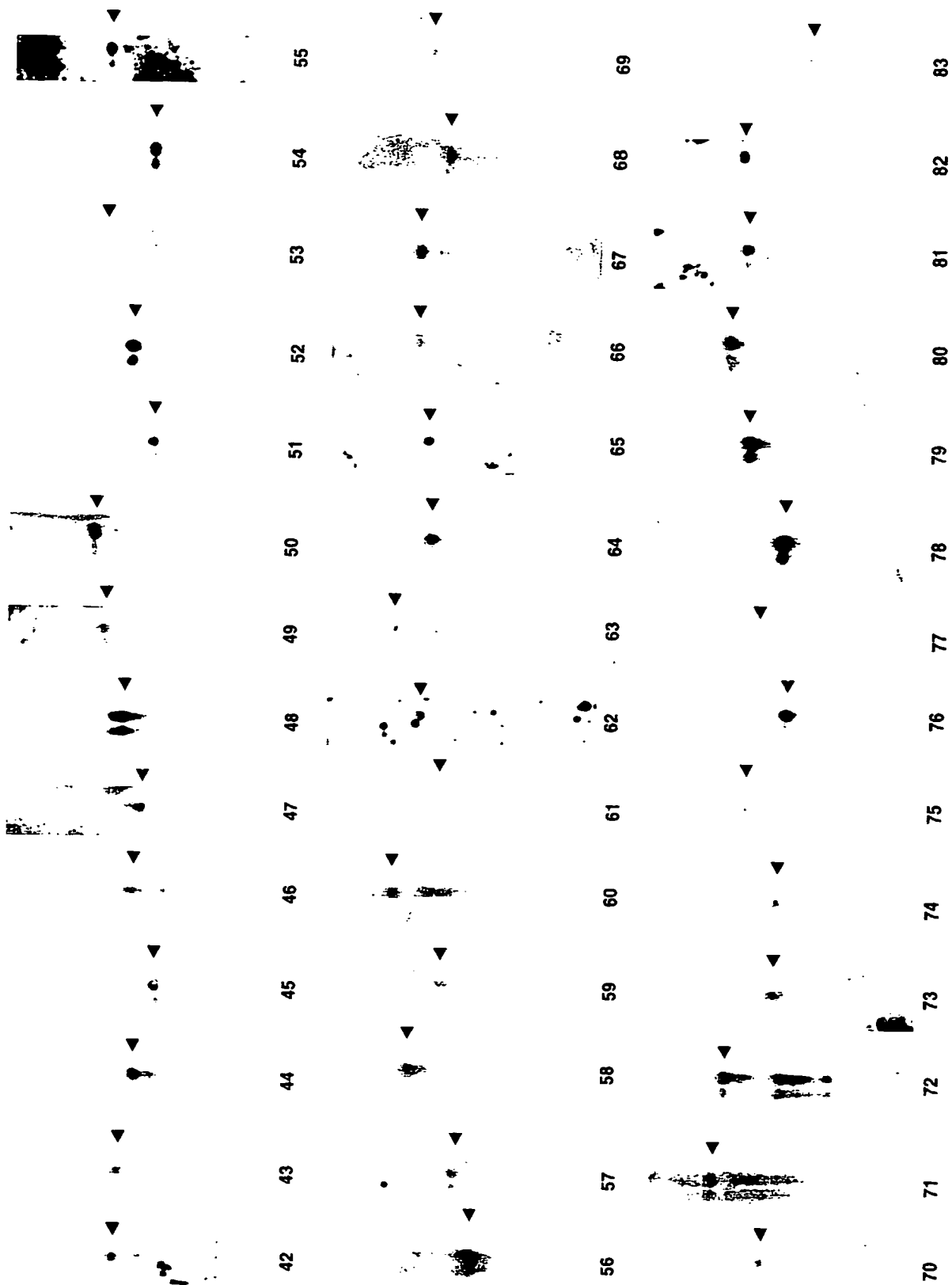


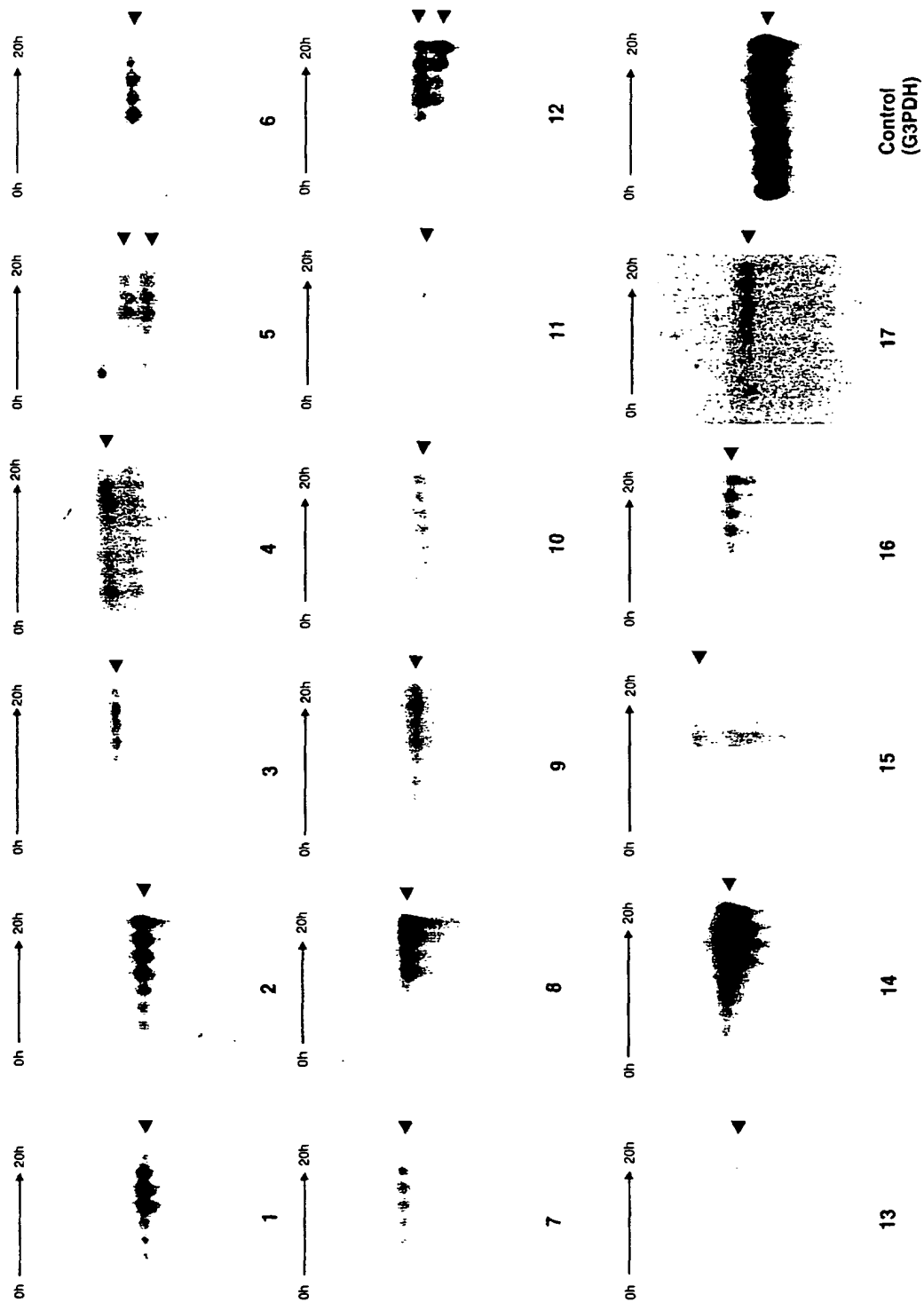
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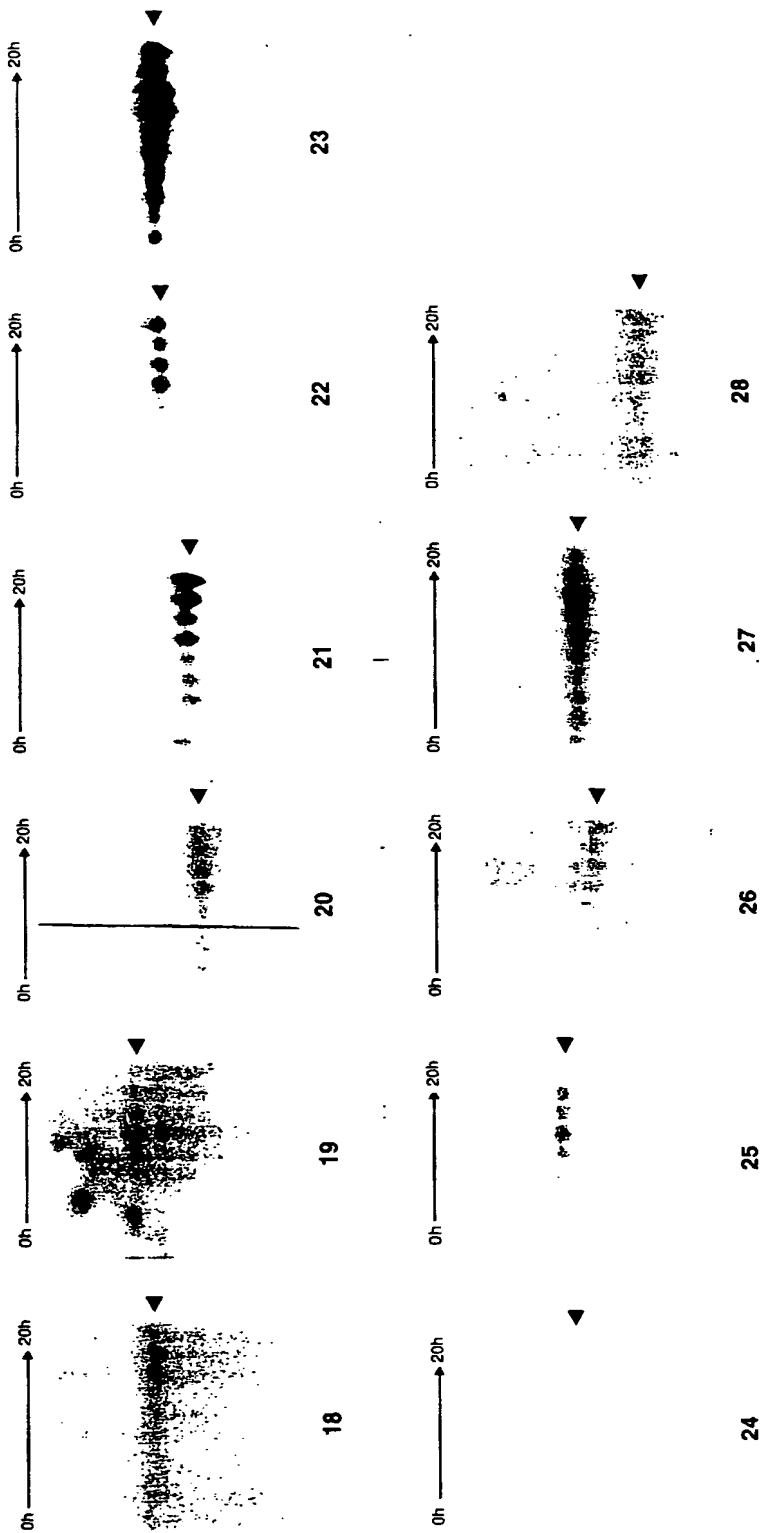




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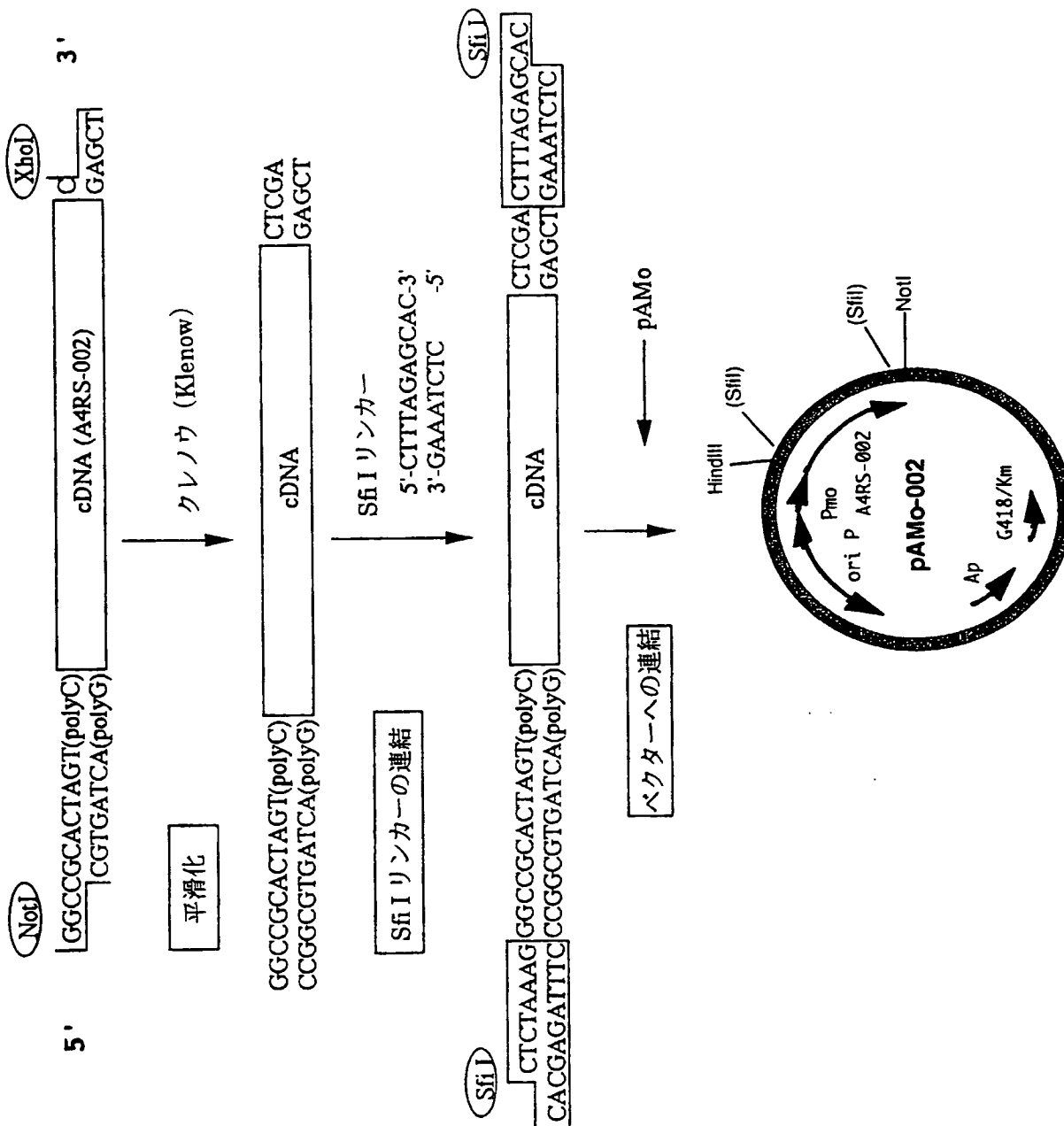


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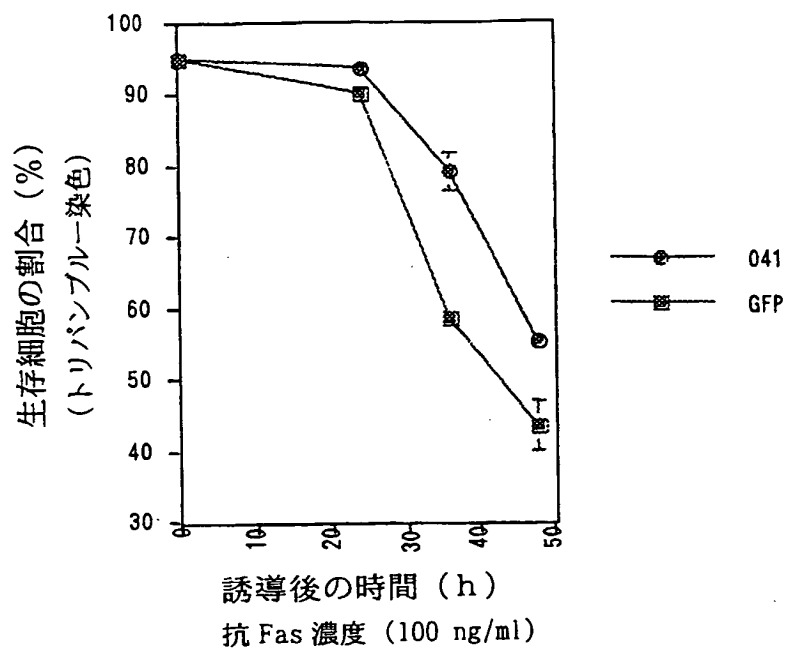
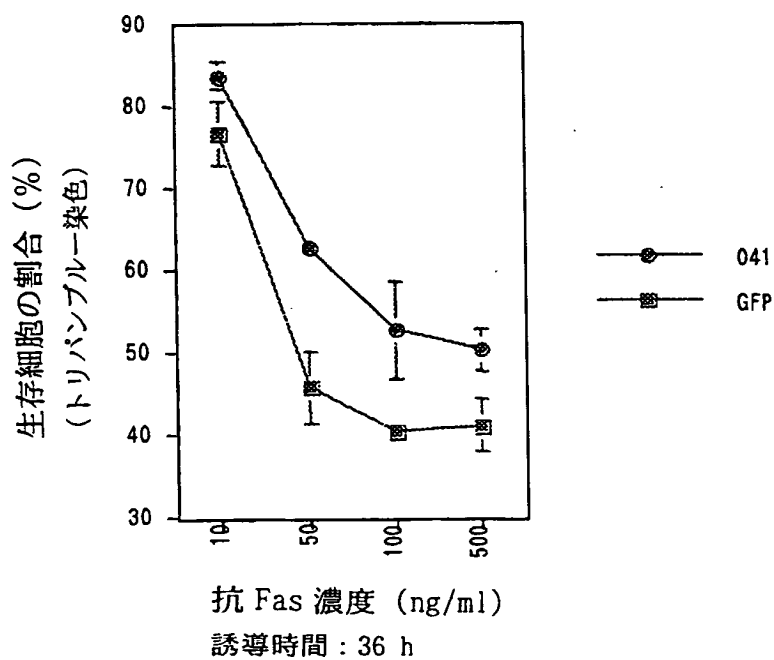
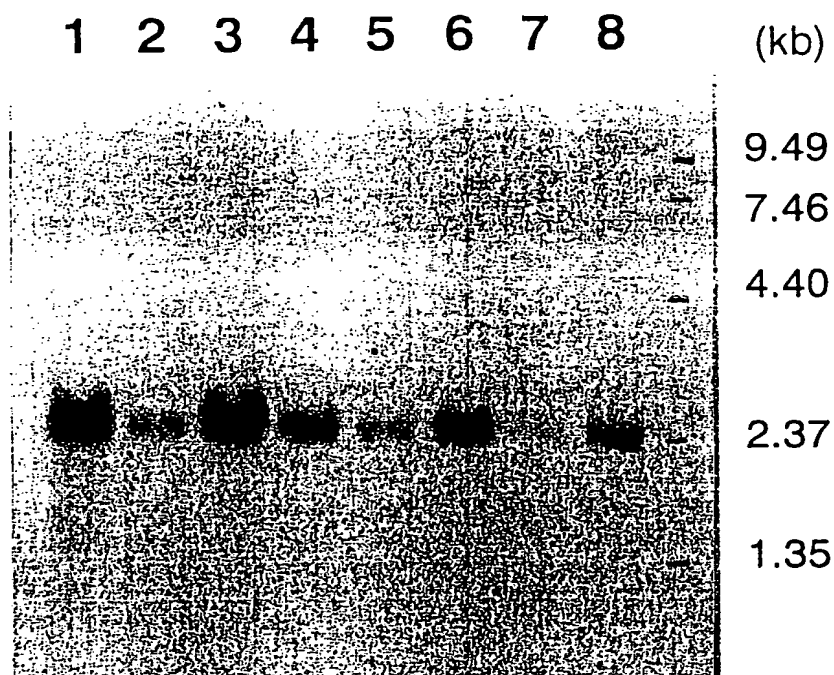


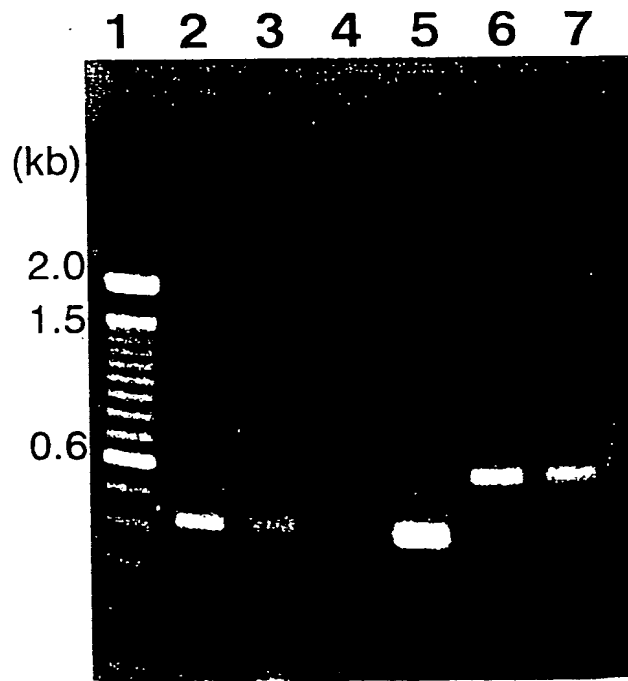
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☒ 7A



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☒ 8

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 Gly His Met His Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro Arg Phe  
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 Lys Asp Phe Gln Arg Met Tyr Arg Asp Ala Gln Glu Arg Gly Leu Asn  
 290 295 300  
 Pro Cys Glu Val Gly Thr Asp  
 305 310

&lt;210&gt; 5

&lt;211&gt; 2820

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (49).. (2664)

&lt;400&gt; 5

ctcccaaagc agaattgcag ctgccgccgc cgccacctcc aggccact atg gcg cct 57

Met Ala Pro

1

ggg gct gcc cag gag ctt cag gcc aag ttg gca gag atc gga gct ccg 105

Gly Ala Ala Gln Glu Leu Gln Ala Lys Leu Ala Glu Ile Gly Ala Pro

5

10

15

atc cag ggt aat cgc gag gag ctg gtg gag cgg ctg cag agc tac acc 153

Ile Gln Gly Asn Arg Glu Glu Leu Val Glu Arg Leu Gln Ser Tyr Thr

20

25

30

35

cgc cag act ggc atc gtg ctg aat cgg ccg gtt ttg aga ggg gaa gat 201

Arg Gln Thr Gly Ile Val Leu Asn Arg Pro Val Leu Arg Gly Glu Asp

40

45

50

ggg gac aaa gcc gct cca cct ccc atg tcg gca cag ctc cct gga att 249

Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu Pro Gly Ile

55

60

65

ccc atg cca cca cca cct ttg gga ctc ccc cct ctg cag cct cct ccg 297

Pro Met Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln Pro Pro Pro

70

75

80

cca ccc cca cca cct cca cca ggc ctt ggc ctt ggc ttt cct atg gcc 345

Pro Pro Pro Pro Pro Pro Pro Gly Leu Gly Leu Gly Phe Pro Met Ala  
 85 90 95  
 cac cca cca aat ttt ggg ccc ccg cct cct ctc cgt gtg ggt gag cca 393  
 His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val Gly Glu Pro  
 100 105 110 115  
 gtg gca ctg tca gag gag gag cgg ctg aag ttg gct cag cag cag gcg 441  
 Val Ala Leu Ser Glu Glu Glu Arg Leu Lys Leu Ala Gln Gln Gln Ala  
 120 125 130  
 gca ttg ctg atg cag cag gag gag cgt gcc aag cag cag gga gat cat 489  
 Ala Leu Leu Met Gln Gln Glu Glu Arg Ala Lys Gln Gln Gly Asp His  
 135 140 145  
 tcg ctg aag gaa cat gag ctc ttg gag cag cag aag cgg gca gct gtg 537  
 Ser Leu Lys Glu His Glu Leu Leu Glu Gln Gln Lys Arg Ala Ala Val  
 150 155 160  
 tta ctg gag cag gaa cga cag cag gag att gcc aag atg ggc acc cca 585  
 Leu Leu Glu Gln Glu Arg Gln Gln Glu Ile Ala Lys Met Gly Thr Pro  
 165 170 175  
 gtc cct cgg ccc cca caa gac atg ggc cag att ggt gtg cgc act cct 633  
 Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val Arg Thr Pro  
 180 185 190 195  
 ctg ggt cct cga gla gct gct cca gtg ggc cca gtg ggc ccc act cct 681  
 Leu Gly Pro Arg Val Ala Ala Pro Val Gly Pro Val Gly Pro Thr Pro  
 200 205 210  
 aca gtt ttg ccc atg gga gcc cct gtt ccc cgg cct cgt ggt ccc cca 729  
 Thr Val Leu Pro Met Gly Ala Pro Val Pro Arg Pro Arg Gly Pro Pro  
 215 220 225

ccg ccc cct gga gat gag aac aga gag atg gat gac ccc tct gtg ggc 777  
 Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro Ser Val Gly  
 230 235 240  
 ccc aag atc ccc cag gct ttg gag aag atc ctg cag ctg aag gag agc 825  
 Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu Lys Glu Ser  
 245 250 255  
 cgc cag gaa gag atg aat tct cag cag gag gaa gag gaa atg gaa aca 873  
 Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Met Glu Thr  
 260 265 270 275  
 gat gct cgc tcg tcc ctg ggc cag tca gcg tca gag act gag gag gac 921  
 Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr Glu Glu Asp  
 280 285 290  
 aca gtg tcc gta tct aaa aag gag aaa aac cgg aag cgt agg aac cga 969  
 Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg Arg Asn Arg  
 295 300 305  
 aag aag aag aaa aag ccc cag cgg gtg cga ggg gtg tcc tct gag agc 1017  
 Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser Ser Glu Ser  
 310 315 320  
 tct ggg gac cgg gag aaa gac tca acc cgg tcc cgt ggc tct gat tcc 1065  
 Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly Ser Asp Ser  
 325 330 335  
 cca gca gct gat gtt gag att gag tat gtg act gaa gaa cct gaa att 1113  
 Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu Pro Glu Ile  
 340 345 350 355  
 tac gag ccc aac ttt atc ttc ttt aag agg atc ttt gag gct ttt aag 1161  
 Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu Ala Phe Lys  
 360 365 370

ctc act gat gat gtg aag aag gag aaa gag aaa gag cca gag aaa ctt 1209  
 Leu Thr Asp Asp Val Lys Lys Glu Lys Glu Lys Glu Pro Glu Lys Leu  
 375 380 385  
 gac aaa ctg gag aac tct gca gcc ccc aag aag aag gga ttt gaa gag 1257  
 Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly Phe Glu Glu  
 390 395 400  
 gag cac aag gac agt gat gat gac agc agt gat gac gag cag gaa aag 1305  
 Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu Gln Glu Lys  
 405 410 415  
 aag cca gaa gcc ccc aag ctg tcc aag aag aag ttg cgc cga atg aac 1353  
 Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg Arg Met Asn  
 420 425 430 435  
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 Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg Pro Asp Val  
 440 445 450  
 gtg gag atg cac gat gtg aca gcg cag gac cct aag ctc ttg gtt cac 1449  
 Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu Leu Val His  
 455 460 465  
 ctc aag gcc act cgg aac tct gtg cct gtg cca cgc cac tgg tgt ttt 1497  
 Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His Trp Cys Phe  
 470 475 480  
 aag cgc aaa tac ctg cag ggc aaa cgg ggc att gag aag ccc ccc ttc 1545  
 Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys Pro Pro Phe  
 485 490 495  
 gag ctg cca gac ttc atc aaa cgc aca ggc atc cag gag atg cga gag 1593  
 Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu Met Arg Glu

500	505	510	515	
gcc ctg cag gag aag gaa gaa cag aag acc atg aag tca aaa atg cga				1641
Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser Lys Met Arg				
	520	525	530	
gag aaa gtt cgg cct aag atg ggc aaa att gac atc gac tac cag aaa				1689
Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp Tyr Gln Lys				
	535	540	545	
ctg cat gat gcc ttc ttc aag tgg cag acc aag cca aag ctg acc atc				1737
Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys Leu Thr Ile				
	550	555	560	
cat ggg gac ctg tac tat gag ggg aag gag ttc gag aca cga ctg aag				1785
His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr Arg Leu Lys				
	565	570	575	
gag aag aag cca gga gat ctg tct gat gag cta agg att tcc ttg ggg				1833
Glu Lys Lys Pro Gly Asp Leu Ser Asp Glu Leu Arg Ile Ser Leu Gly				
580	585	590	595	
atg cca gta gga cca aat gcc cac aag gtc cct ccc cca tgg ctg att				1881
Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro Trp Leu Ile				
	600	605	610	
gcc atg cag cga tat gga cca ccc cca tcg tat ccc aac ctg aaa atc				1929
Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn Leu Lys Ile				
	615	620	625	
cct ggg ctg aac tcg ccc atc cct gag agc tgt tcc ttt ggg tac cat				1977
Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe Gly Tyr His				
	630	635	640	
gct ggt ggc tgg ggc aaa cct cca gtg gat gag act ggg aaa ccg ctc				2025
Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly Lys Pro Leu				

645	650	655	
tal ggg gac gtg ttt gga acc aat gct gct gaa ttt cag acc aag act	2073		
Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln Thr Lys Thr			
660	665	670	675
gag gaa gaa gag att gat cgg acc cct tgg ggg gaa ctg gaa cca tct	2121		
Glu Glu Glu Glu Ile Asp Arg Thr Pro Trp Gly Glu Leu Glu Pro Ser			
680	685	690	
gat gaa gaa tcc tca gaa gaa gag gaa gag gaa gaa agt gat gaa gac	2169		
Asp Glu Glu Ser Ser Glu Glu Glu Glu Glu Glu Glu Ser Asp Glu Asp			
695	700	705	
aaa cca gat gag aca ggc ttt att acc cct gca gac agt ggc ctt atc	2217		
Lys Pro Asp Glu Thr Gly Phe Ile Thr Pro Ala Asp Ser Gly Leu Ile			
710	715	720	
act cct gga ggc ttt tca tca gtg cct gct gga atg gag acc cct gaa	2265		
Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu Thr Pro Glu			
725	730	735	
ctc att gag ctg agg aag aag aag att gag gag gcg atg gac gga agt	2313		
Leu Ile Glu Leu Arg Lys Lys Lys Ile Glu Glu Ala Met Asp Gly Ser			
740	745	750	755
gag aca cct cag ctc ttc act gtg ttg cca gag aag aga aca gcc act	2361		
Glu Thr Pro Gln Leu Phe Thr Val Leu Pro Glu Lys Arg Thr Ala Thr			
760	765	770	
gtt gga ggg gcc atg atg gga tca acc cac att tat gac atg tcc acg	2409		
Val Gly Gly Ala Met Met Gly Ser Thr His Ile Tyr Asp Met Ser Thr			
775	780	785	
gtt atg agc cgg aag ggc ccg gct cct gag ctg caa ggt gtg gaa gtg	2457		

Val Met Ser Arg Lys Gly Pro Ala Pro Glu Leu Gln Gly Val Glu Val  
 790 795 800  
 gcg ctg gcg cct gaa gag ttg gag ctg gat cct atg gcc atg acc cag 2505  
 Ala Leu Ala Pro Glu Glu Leu Glu Leu Asp Pro Met Ala Met Thr Gln  
 805 810 815  
 aag tat gag gag cat gtg cgg gag cag cag gct caa gta gag aag gag 2553  
 Lys Tyr Glu Glu His Val Arg Glu Gln Gln Ala Gln Val Glu Lys Glu  
 820 825 830 835  
 gac ttc agt gac atg gtg gct gag cac gct gcc aaa cag aag caa aaa 2601  
 Asp Phe Ser Asp Met Val Ala Glu His Ala Ala Lys Gln Lys Gln Lys  
 840 845 850  
 aaa cgg aaa gct cag ccc cag gac agc cgt ggg ggc agc aag aaa tat 2649  
 Lys Arg Lys Ala Gln Pro Gln Asp Ser Arg Gly Gly Ser Lys Lys Tyr  
 855 860 865  
 aag gag ttc aag ttt taggtccct cacactagcc ctttttttgg ccctacgtct 2704  
 Lys Glu Phe Lys Phe  
 870  
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&lt;210&gt; 6

&lt;211&gt; 872

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

Met Ala Pro Gly Ala Ala Gln Glu Leu Gln Ala Lys Leu Ala Glu Ile

1

5

10

15



Gly Ala Pro Ile Gln Gly Asn Arg Glu Glu Leu Val Glu Arg Leu Gln  
 20 25 30  
 Ser Tyr Thr Arg Gln Thr Gly Ile Val Leu Asn Arg Pro Val Leu Arg  
 35 40 45  
 Gly Glu Asp Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu  
 50 55 60  
 Pro Gly Ile Pro Met Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln  
 65 70 75 80  
 Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Leu Gly Leu Gly Phe  
 85 90 95  
 Pro Met Ala His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val  
 100 105 110  
 Gly Glu Pro Val Ala Leu Ser Glu Glu Glu Arg Leu Lys Leu Ala Gln  
 115 120 125  
 Gln Gln Ala Ala Leu Leu Met Gln Gln Glu Glu Arg Ala Lys Gln Gln  
 130 135 140  
 Gly Asp His Ser Leu Lys Glu His Glu Leu Leu Glu Gln Gln Lys Arg  
 145 150 155 160  
 Ala Ala Val Leu Leu Glu Gln Glu Arg Gln Gln Glu Ile Ala Lys Met  
 165 170 175  
 Gly Thr Pro Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val  
 180 185 190  
 Arg Thr Pro Leu Gly Pro Arg Val Ala Ala Pro Val Gly Pro Val Gly  
 195 200 205  
 Pro Thr Pro Thr Val Leu Pro Met Gly Ala Pro Val Pro Arg Pro Arg  
 210 215 220  
 Gly Pro Pro Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro

225                      230                      235                      240  
Ser Val Gly Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu  
                         245                      250                      255  
Lys Glu Ser Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Glu  
                         260                      265                      270  
Met Glu Thr Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr  
                         275                      280                      285  
Glu Glu Asp Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg  
                         290                      295                      300  
Arg Asn Arg Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser  
305                      310                      315                      320  
Ser Glu Ser Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly  
                         325                      330                      335  
Ser Asp Ser Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu  
                         340                      345                      350  
Pro Glu Ile Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu  
                         355                      360                      365  
Ala Phe Lys Leu Thr Asp Asp Val Lys Lys Glu Lys Glu Lys Glu Pro  
                         370                      375                      380  
Glu Lys Leu Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly  
385                      390                      395                      400  
Phe Glu Glu Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu  
                         405                      410                      415  
Gln Glu Lys Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg  
                         420                      425                      430  
Arg Met Asn Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg

435 440 445  
Pro Asp Val Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu  
450 455 460  
Leu Val His Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His  
465 470 475 480  
Trp Cys Phe Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys  
485 490 495  
Pro Pro Phe Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu  
500 505 510  
Met Arg Glu Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser  
515 520 525  
Lys Met Arg Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp  
530 535 540  
Tyr Gln Lys Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys  
545 550 555 560  
Leu Thr Ile His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr  
565 570 575  
Arg Leu Lys Glu Lys Lys Pro Gly Asp Leu Ser Asp Glu Leu Arg Ile  
580 585 590  
Ser Leu Gly Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro  
595 600 605  
Trp Leu Ile Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn  
610 615 620  
Leu Lys Ile Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe  
625 630 635 640  
Gly Tyr His Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly  
645 650 655

Lys Pro Leu Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln  
 660 665 670  
 Thr Lys Thr Glu Glu Glu Glu Ile Asp Arg Thr Pro Trp Gly Glu Leu  
 675 680 685  
 Glu Pro Ser Asp Glu Glu Ser Ser Glu Glu Glu Glu Glu Glu Ser  
 690 695 700  
 Asp Glu Asp Lys Pro Asp Glu Thr Gly Phe Ile Thr Pro Ala Asp Ser  
 705 710 715 720  
 Gly Leu Ile Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu  
 725 730 735  
 Thr Pro Glu Leu Ile Glu Leu Arg Lys Lys Lys Ile Glu Glu Ala Met  
 740 745 750  
 Asp Gly Ser Glu Thr Pro Gln Leu Phe Thr Val Leu Pro Glu Lys Arg  
 755 760 765  
 Thr Ala Thr Val Gly Gly Ala Met Met Gly Ser Thr His Ile Tyr Asp  
 770 775 780  
 Met Ser Thr Val Met Ser Arg Lys Gly Pro Ala Pro Glu Leu Gln Gly  
 785 790 795 800  
 Val Glu Val Ala Leu Ala Pro Glu Glu Leu Glu Leu Asp Pro Met Ala  
 805 810 815  
 Met Thr Gln Lys Tyr Glu Glu His Val Arg Glu Gln Gln Ala Gln Val  
 820 825 830  
 Glu Lys Glu Asp Phe Ser Asp Met Val Ala Glu His Ala Ala Lys Gln  
 835 840 845  
 Lys Gln Lys Lys Arg Lys Ala Gln Pro Gln Asp Ser Arg Gly Gly Ser  
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Lys Lys Tyr Lys Glu Phe Lys Phe

865

870

<210> 7

<211> 2433

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (214).. (1146)

<400> 7

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 ctggtccccc gaggtctctg ccagctgac agtgttcttg gcactgctca aaggtcccag 180  
 cagctggggt tccccgtcag cccgtgagcg gcc atg tcc aac ccc agc gcc cca 234

Met Ser Asn Pro Ser Ala Pro

1

5

cca cca tat gaa gac cgc aac ccc ctg tac cca ggc cct ccg ccc cct 282

Pro Pro Tyr Glu Asp Arg Asn Pro Leu Tyr Pro Gly Pro Pro Pro Pro

10

15

20

ggg ggc tat ggg cag cca tct gtc ctg cca gga ggg tat cct gcc tac 330

Gly Gly Tyr Gly Gln Pro Ser Val Leu Pro Gly Gly Tyr Pro Ala Tyr

25

30

35

cct ggc tac ccg cag cct ggc tac ggt cac cct gct ggc tac cca cag 378

Pro Gly Tyr Pro Gln Pro Gly Tyr Gly His Pro Ala Gly Tyr Pro Gln

40

45

50

55

ccc atg ccc ccc acc cac ccg atg ccc atg aac tac ggc cca ggc cat 426

Pro Met Pro Pro Thr His Pro Met Pro Met Asn Tyr Gly Pro Gly His  
                     60                    65                    70  
 ggc tai gat ggg gag gag aga gcg gtg agt gat agc ttc ggg cct gga 474  
 Gly Tyr Asp Gly Glu Glu Arg Ala Val Ser Asp Ser Phe Gly Pro Gly  
                     75                    80                    85  
 gag tgg gat gac cgg aaa gtg cga cac act ttt atc cga aag gtt tac 522  
 Glu Trp Asp Asp Arg Lys Val Arg His Thr Phe Ile Arg Lys Val Tyr  
                     90                    95                    100  
 tcc atc atc tcc gtg cag ctg ctc atc act gtg gcc atc att gct atc 570  
 Ser Ile Ile Ser Val Gln Leu Leu Ile Thr Val Ala Ile Ile Ala Ile  
                     105                    110                    115  
 ttc acc ttt gtg gaa cct gtc agc gcc ttt gtg agg aga aat gtg gct 618  
 Phe Thr Phe Val Glu Pro Val Ser Ala Phe Val Arg Arg Asn Val Ala  
                     120                    125                    130                    135  
 gtc tac tac gtg tcc tai gct gtc ttc gtt gtc acc tac ctg atc ctt 666  
 Val Tyr Tyr Val Ser Tyr Ala Val Phe Val Val Thr Tyr Leu Ile Leu  
                     140                    145                    150  
 gcc tgc tgc cag gga ccc aga cgc cgt ttc cca tgg aac atc att ctg 714  
 Ala Cys Cys Gln Gly Pro Arg Arg Arg Phe Pro Trp Asn Ile Ile Leu  
                     155                    160                    165  
 ctg acc ctt ttt act ttt gcc atg ggc ttc atg acg ggc acc att tcc 762  
 Leu Thr Leu Phe Thr Phe Ala Met Gly Phe Met Thr Gly Thr Ile Ser  
                     170                    175                    180  
 agt atg tac caa acc aaa gcc gtc atc att gca atg atc atc act gcg 810  
 Ser Met Tyr Gln Thr Lys Ala Val Ile Ile Ala Met Ile Ile Thr Ala  
                     185                    190                    195  
 gtg gla tcc att tca gtc acc atc ttc tgc ttt cag acc aag gtg gac 858

Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe Gln Thr Lys Val Asp  
 200 205 210 215  
 ttc acc tcg tgc aca ggc ctc ttc tgt gtc ctg gga att gtc ctc ctg 906  
 Phe Thr Ser Cys Thr Gly Leu Phe Cys Val Leu Gly Ile Val Leu Leu  
 220 225 230  
 gtg act ggg att gtc act agc att gtg ctc tac ttc caa tac gtt tac 954  
 Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr  
 235 240 245  
 tgg ctc cac atg ctc tat gct gct ctg ggg gcc att tgt ttc acc ctg 1002  
 Trp Leu His Met Leu Tyr Ala Ala Leu Gly Ala Ile Cys Phe Thr Leu  
 250 255 260  
 ttc ctg gct tac gac aca cag ctg gtc ctg ggg aac cgg aag cac acc 1050  
 Phe Leu Ala Tyr Asp Thr Gln Leu Val Leu Gly Asn Arg Lys His Thr  
 265 270 275  
 atc agc ccc gag gac tac atc act ggc gcc ctg cag att tac aca gac 1098  
 Ile Ser Pro Glu Asp Tyr Ile Thr Gly Ala Leu Gln Ile Tyr Thr Asp  
 280 285 290 295  
 atc atc tac atc ttc acc ttt gtg ctg cag ctg atg ggg gat cgc aat 1146  
 Ile Ile Tyr Ile Phe Thr Phe Val Leu Gln Leu Met Gly Asp Arg Asn  
 300 305 310  
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 ggccciatga ctgtggtctg ggctttaggc ccttttctt ccccttgagt aacatgccca 1266  
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 aagaigtgtc ttctccccgc cacctactgt atgacaccac attcttccia acagctgggg 1446  
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gacttcaagg tcacgagglt cccclccac ctcgtcaca ggcttcttga ctacgtagtt 1566  
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 gaagacttct gggttctttc ctctgctaa cccaggagg gtcctaagag gaaggtagct 2166  
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<210> 8

<211> 311

<212> PRT

<213> Homo sapiens

<400> 8

Met Ser Asn Pro Ser Ala Pro Pro Pro Tyr Glu Asp Arg Asn Pro Leu

1 5 10 15

Tyr Pro Gly Pro Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu

20 25 30

Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly



35	40	45	
His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro			
50	55	60	
Met Asn Tyr Gly Pro Gly His Gly Tyr Asp Gly Glu Glu Arg Ala Val			
65	70	75	80
Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp Arg Lys Val Arg His			
85	90	95	
Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu Ile			
100	105	110	
Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser Ala			
115	120	125	
Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe			
130	135	140	
Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg			
145	150	155	160
Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly			
165	170	175	
Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile			
180	185	190	
Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe			
195	200	205	
Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys			
210	215	220	
Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val			
225	230	235	240
Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu			
245	250	255	

Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val

260

265

270

Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly

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Met Pro Glu Lys Arg Pro Phe Glu Arg

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ctg cct gcc gat gtc tcc ccc atc aac tac agc ctt tgc ctc aag ccc 160

Leu Pro Ala Asp Val Ser Pro Ile Asn Tyr Ser Leu Cys Leu Lys Pro

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15

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25

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Asp Leu Leu Asp Phe Thr Phe Glu Gly Lys Leu Glu Ala Ala Ala Gln

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 Ser Asn Met Asn Val Ile Asp Arg Lys Pro Tyr Pro Asp Asp Glu Asn

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Asp Tyr Phe Asn Val Pro Tyr Pro Leu Pro Lys Ile Asp Leu Ile Ala				
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Ile Ala Asp Phe Ala Ala Gly Ala Met Glu Asn Trp Gly Leu Val Thr				
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Tyr Arg Glu Thr Ala Leu Leu Ile Asp Pro Lys Asn Ser Cys Ser Ser				
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Ser Arg Gln Trp Val Ala Leu Val Val Gly His Glu Leu Ala His Gln				
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cgt gcc cag gag ctt gac gcc tta gat aac agc cat cct att gaa gtc			1216
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Ser Val Gly His Pro Ser Glu Val Asp Glu Ile Phe Asp Ala Ile Ser			
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Ile Val Met Asn Cys Ala Asp Ile Asp Ile Ile Thr Ala Ser Tyr Ala

50 55 60

Pro Glu Gly Asp Glu Glu Ile His Ala Thr Gly Phe Asn Tyr Gln Asn

65 70 75 80

Glu Asp Glu Lys Val Thr Leu Ser Phe Pro Ser Thr Leu Gln Thr Gly

85 90 95

Thr Gly Thr Leu Lys Ile Asp Phe Val Gly Glu Leu Asn Asp Lys Met

100 105 110

Lys Gly Phe Tyr Arg Ser Lys Tyr Thr Thr Pro Ser Gly Glu Val Arg

115 120 125

Tyr Ala Ala Val Thr Gln Phe Glu Ala Thr Asp Ala Arg Arg Ala Phe

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Pro Cys Trp Asp Glu Pro Ala Ile Lys Ala Thr Phe Asp Ile Ser Leu

145 150 155 160

Val Val Pro Lys Asp Arg Val Ala Leu Ser Asn Met Asn Val Ile Asp

165 170 175

Arg Lys Pro Tyr Pro Asp Asp Glu Asn Leu Val Glu Val Lys Phe Ala

180 185 190

Arg Thr Pro Val Met Ser Thr Tyr Leu Val Ala Phe Val Val Gly Glu

195 200 205  
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275 280 285  
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305 310 315 320  
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325 330 335  
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370 375 380  
Val Asp Glu Ile Phe Asp Ala Ile Ser Tyr Ser Lys Gly Ala Ser Val  
385 390 395 400  
Ile Arg Met Leu His Asp Tyr Ile Gly Asp Lys Asp Phe Lys Lys Gly  
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545 550 555 560  
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565 570 575  
Asp Leu Phe Ser Leu Ala Arg Ala Gly Ile Ile Ser Thr Val Glu Val  
580 585 590  
Leu Lys Val Met Glu Ala Phe Val Asn Glu Pro Asn Tyr Thr Val Trp  
595 600 605  
Ser Asp Leu Ser Cys Asn Leu Gly Ile Leu Ser Thr Leu Leu Ser His  
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Thr Asp Phe Tyr Glu Glu Ile Gln Glu Phe Val Lys Asp Val Phe Ser  
625 630 635 640  
Pro Ile Gly Glu Arg Leu Gly Trp Asp Pro Lys Pro Gly Glu Gly His  
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Lys Leu His Lys Gln Ala Asp Met Gln Glu Glu Lys Asn Arg Ile Glu  
725 730 735  
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740 745 750  
Thr Phe Ala Leu Ser Glu Glu Val Arg Pro Gln Asp Thr Val Ser Val  
755 760 765  
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770 775 780  
Lys Phe Ile Lys Asp Asn Trp Glu Glu Leu Tyr Asn Arg Tyr Gln Gly  
785 790 795 800  
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820 825 830  
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&lt;211&gt; 2007

&lt;212&gt; DNA

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&lt;220&gt;

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&lt;222&gt; (1124).. (1330)

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Met Asp Lys Gln

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Glu Phe Gly Asp Gln

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<210> 13

<211> 1953

<212> DNA

<213> Homo sapiens



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&lt;222&gt; (135).. (1850)

&lt;400&gt; 13

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ccaacctgcc  ggcc  atg  gag  acc  ccg  tcc  cag  cgg  cgc  gcc  acc  cgc  agc  170
          Met  Glu  Thr  Pro  Ser  Gln  Arg  Arg  Ala  Thr  Arg  Ser
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ggg  gcg  cag  gcc  agc  tcc  act  ccg  ctg  tcg  ccc  acc  cgc  atc  acc  cgg  218
Gly  Ala  Gln  Ala  Ser  Ser  Thr  Pro  Leu  Ser  Pro  Thr  Arg  Ile  Thr  Arg
          15                20                25
ctg  cag  gag  aag  gag  gac  ctg  cag  gag  ctc  aat  gat  cgc  ttg  gcg  gtc  266
Leu  Gln  Glu  Lys  Glu  Asp  Leu  Gln  Glu  Leu  Asn  Asp  Arg  Leu  Ala  Val
          30                35                40
tac  atc  gac  cgt  gtg  cgc  tcg  ctg  gaa  acg  gag  aac  gca  ggg  ctg  cgc  314
Tyr  Ile  Asp  Arg  Val  Arg  Ser  Leu  Glu  Thr  Glu  Asn  Ala  Gly  Leu  Arg
          45                50                55                60
ctt  cgc  atc  acc  gag  tct  gaa  gag  gtg  gtc  agc  cgc  gag  gtg  tcc  ggc  362
Leu  Arg  Ile  Thr  Glu  Ser  Glu  Glu  Val  Val  Ser  Arg  Glu  Val  Ser  Gly
                65                70                75
atc  aag  gcc  gcc  tac  gag  gcc  gag  ctc  ggg  gat  gcc  cgc  aag  acc  ctt  410
Ile  Lys  Ala  Ala  Tyr  Glu  Ala  Glu  Leu  Gly  Asp  Ala  Arg  Lys  Thr  Leu
                80                85                90
gac  tca  gta  gcc  aag  gag  cgc  gcc  cgc  ctg  cag  ctg  gag  ctg  agc  aaa  458
Asp  Ser  Val  Ala  Lys  Glu  Arg  Ala  Arg  Leu  Gln  Leu  Glu  Leu  Ser  Lys

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95	100	105	
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Val Arg Glu Glu Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu			
110	115	120	
ggc gac ctg ata gct gct cag gct cgg ctg aag gac ctg gag gct ctg	554		
Gly Asp Leu Ile Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu			
125	130	135	140
ctg aac tcc aag gag gcc gca ctg agc act gct ctc agt gag aag cgc	602		
Leu Asn Ser Lys Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg			
145	150	155	
acg ctg gag ggc gag ctg cat gat ctg cgg ggc cag gtg gcc aag ctt	650		
Thr Leu Glu Gly Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu			
160	165	170	
gag gca gcc cta ggt gag gcc aag aag caa ctt cag gat gag atg ctg	698		
Glu Ala Ala Leu Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu			
175	180	185	
cgg cgg gtg gat gct gag aac agg ctg cag acc atg aag gag gaa ctg	746		
Arg Arg Val Asp Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu			
190	195	200	
gac ttc cag aag aac atc tac agt gag gag ctg cgt gag acc aag cgc	794		
Asp Phe Gln Lys Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg			
205	210	215	220
cgt cat gag acc cga ctg gtg gag att gac aat ggg aag cag cgt gag	842		
Arg His Glu Thr Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu			
225	230	235	
ttt gag agc cgg ctg gcg gat gcg ctg cag gaa ctg cgg gcc cag cat	890		
Phe Glu Ser Arg Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His			

240	245	250	
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Glu Asp Gln Val Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser			
255	260	265	
gcc aag ctg gac aat gcc agg cag tct gct gag agg aac agc aac ctg			986
Ala Lys Leu Asp Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu			
270	275	280	
gtg ggg gct gcc cac gag gag ctg cag cag tcg cgc atc cgc atc gac			1034
Val Gly Ala Ala His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp			
285	290	295	300
agc ctc tct gcc cag ctc agc cag ctc cag aag cag ctg gca gcc aag			1082
Ser Leu Ser Ala Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys			
305	310	315	
gag gcg aag ctt cga gac ctg gag gac tca ctg gcc cgt gag cgg gac			1130
Glu Ala Lys Leu Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp			
320	325	330	
acc agc cgg cgg ctg ctg gcg gaa aag gag cgg gag atg gcc gag atg			1178
Thr Ser Arg Arg Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met			
335	340	345	
cgg gca agg atg cag cag cag ctg gac gag tac cag gag ctt ctg gac			1226
Arg Ala Arg Met Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp			
350	355	360	
atc aag ctg gcc ctg gac atg gag atc cac gcc tac cgc aag ctc ttg			1274
Ile Lys Leu Ala Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu			
365	370	375	380
gag ggc gag gag gag agg cta cgc ctg tcc ccc agc cct acc tcg cag			1322

Glu Gly Glu Glu Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln  
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 Arg Ser Arg Gly Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly  
 400 405 410  
 ggc agc gtc acc aaa aag cgc aaa ctg gag tcc act gag agc cgc agc 1418  
 Gly Ser Val Thr Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser  
 415 420 425  
 agc ttc tca cag cac gca cgc act agc ggg cgc gtg gcc gtg gag gag 1466  
 Ser Phe Ser Gln His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu  
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 Val Asp Glu Glu Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu  
 445 450 455 460  
 gac cag tcc atg ggc aat tgg cag atc aag cgc cag aat gga gat gat 1562  
 Asp Gln Ser Met Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp  
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 Pro Leu Leu Thr Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly  
 480 485 490  
 cag gtg gtg acg atc tgg gct gca gga gct ggg gcc acc cac agc ccc 1658  
 Gln Val Val Thr Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro  
 495 500 505  
 cct acc gac ctg gtg tgg aag gca cag aac acc tgg ggc tgc ggg aac 1706  
 Pro Thr Asp Leu Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn  
 510 515 520  
 agc ctg cgt acg gct ctc atc aac tcc act ggg gaa gaa gtg gcc atg 1754

Ser Leu Arg Thr Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met  
 525                      530                      535                      540  
 cgc aag ctg gtg cgc tca gtg act gtg gtt gag gac gac gag gat gag 1802  
 Arg Lys Leu Val Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu  
                          545                      550                      555  
 gat gga gat gac ctg ctc cat cac cac cac gtg agt ggt agc cgc cgc 1850  
 Asp Gly Asp Asp Leu Leu His His His His Val Ser Gly Ser Arg Arg  
                          560                      565                      570  
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<210> 14

<211> 572

<212> PRT

<213> Homo sapiens

<400> 14

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                          20                      25                      30  
 Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg  
                          35                      40                      45  
 Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr  
                          50                      55                      60  
 Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala  
   65                      70                      75                      80  
 Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala

	85	90	95
Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu			
100	105	110	
Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile			
115	120	125	
Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys			
130	135	140	
Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly			
145	150	155	160
Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu			
165	170	175	
Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp			
180	185	190	
Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys			
195	200	205	
Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr			
210	215	220	
Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg			
225	230	235	240
Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val			
245	250	255	
Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp			
260	265	270	
Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala			
275	280	285	
His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala			

290 295 300  
Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu  
305 310 315 320  
Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg  
325 330 335  
Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met  
340 345 350  
Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala  
355 360 365  
Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu  
370 375 380  
Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly  
385 390 395 400  
Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr  
405 410 415  
Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln  
420 425 430  
His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu  
435 440 445  
Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met  
450 455 460  
Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr  
465 470 475 480  
Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr  
485 490 495  
Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu  
500 505 510

Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr

515

520

525

Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val

530

535

540

Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp

545

550

555

560

Leu Leu His His His His Val Ser Gly Ser Arg Arg

565

570

<210> 15

<211> 2865

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (240).. (1475)

<400> 15

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cgcccccaac tgaagctgca tctcaaagcc gaagattcca gcagcccagg ggatttcaaa 120

gagctcagac tcagaggaac atctgcggag agacccccga agccctctcc agggcagctc 180

tcatccagac gctccgtag tgcagacagg agcgcgcagt ggccccggct cgccgcgcc 239

atg gag cgg atc ccc agc gcg caa cca ccc ccc gcc tgc ctg ccc aaa 287

Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys

1

5

10

15

gca ccg gga ctg gag cac cga gac cta cca ggg atg tac cct gcc cac 335

Ala Pro Gly Leu Glu His Arg Asp Leu Pro Gly Met Tyr Pro Ala His

20

25

30



atg tac caa gtg tac aag tca aga cgg gga ata aag cgg agc gag gac 383  
 Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp  
 35 40 45  
 agc aag gag acc tac aaa ttg ccg cac cgg ctc ttc gag aaa aag aga 431  
 Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg  
 50 55 60  
 cgt gac cgg att aac gag tgc atc gcc cag ctg aag gat ctc cta ccc 479  
 Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro  
 65 70 75 80  
 gaa cat ctc aaa ctt aca act ttg ggt cac ttg gaa aaa gca gtg gtt 527  
 Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val  
 85 90 95  
 ctt gaa ctt acc ttg aag cat glg aaa gca cta aca aac cta att gat 575  
 Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp  
 100 105 110  
 cag cag cag cag aaa atc att gcc ctg cag agt ggt tta caa gct ggt 623  
 Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly  
 115 120 125  
 gag ctg tca ggg aga aat gtc gaa aca ggt caa gag atg ttc tgc tca 671  
 Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser  
 130 135 140  
 ggt ttc cag aca tgt gcc cgg gag gtg ctt cag tat ctg gcc aag cac 719  
 Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His  
 145 150 155 160  
 gag aac act cgg gac ctg aag tct tcg cag ctt gtc acc cac ctc cac 767  
 Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His

165	170	175	
cgg gfg gtc tgc gag ctg ctg cag ggt ggt acc tcc agg aag cca tca	815		
Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser			
180	185	190	
gac cca gct ccc aaa gtg atg gac ttc aag gaa aaa ccc agc tct ccg	863		
Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro			
195	200	205	
gcc aaa ggt tgc gaa ggt cct ggg aaa aac tgc gtg cca gtc atc cag	911		
Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln			
210	215	220	
cgg act ttc gct cac tgc agt ggg gag cag agc ggc agc gac acg gac	959		
Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp			
225	230	235	240
aca gac agt ggc tat gga gga gat tgc gag aag ggc gac ttg cgc agt	1007		
Thr Asp Ser Gly Tyr Gly Gly Asp Ser Glu Lys Gly Asp Leu Arg Ser			
245	250	255	
gag cag ccg tgc ttc aaa agt gac cac gga cgc agg ttc acg atg gga	1055		
Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly			
260	265	270	
gaa agg atc ggc gca att aag caa gag tcc gaa gaa ccc ccc aca aaa	1103		
Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys			
275	280	285	
aag aac cgg atg cag ctt tgc gat gat gaa ggc cat ttc act agc agt	1151		
Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser			
290	295	300	
gac ctg atc agc tcc ccg ttc ctg ggc cca cac cca cac cag cct cct	1199		
Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro			

305                      310                      315                      320  
 ttc tgc ctg ccc ttc tac ctg atc cca cct tca gcg act gcc tac ctg 1247  
 Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu  
                          325                      330                      335  
 ccc atg ctg gag aag tgc tgg tat ccc acc tca gtg cca gtg cta tac 1295  
 Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr  
                          340                      345                      350  
 cca ggc ctc aac gcc tct gcc gca gcc ctc tct agc ttc atg aac cca 1343  
 Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro  
                          355                      360                      365  
 gac aag atc tcg gct ccc ttg ctc atg ccc cag aga ctc cct tct ccc 1391  
 Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro  
                          370                      375                      380  
 ttg cca gct cat ccg tcc gtc gac tct tct gtc ttg ctc caa gct ctg 1439  
 Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu  
 385                      390                      395                      400  
 aag cca atc ccc cct tta aac tta gaa acc aaa gac taaactctct 1485  
 Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp  
                          405                      410  
 aggggatacct gctgcttngc tticctncct cgctacttcc taaaaagcaa ccnnaaagnt 1545  
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 caganncagg gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtatgtgcgt gtgcgtgcac 1665  
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tcaaaagagg gctttccagg gctcagctcc caaccagctg ttaggacccc acccttttgc 1965  
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 ctgctaacat ggggagggla gcagacacig gcatagcacg gtagtggttt ggggaggggt 2085  
 ttccgcaggi ctgctcccca cccctgccic ggaagaataa agagaatgta gttccctact 2145  
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 ntgttncaga tgtttatttg tataattact tgattcacan agngagaaaa antgantgta 2805  
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<210> 16

<211> 412

<212> PRT

<213> Homo sapiens

<400> 16

Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys

1

5

10

15

Ala Pro Gly Leu Glu His Arg Asp Leu Pro Gly Met Tyr Pro Ala His

20

25

30

Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp

35 40 45  
Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg  
50 55 60  
Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro  
65 70 75 80  
Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val  
85 90 95  
Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp  
100 105 110  
Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly  
115 120 125  
Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser  
130 135 140  
Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His  
145 150 155 160  
Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His  
165 170 175  
Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser  
180 185 190  
Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro  
195 200 205  
Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln  
210 215 220  
Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp  
225 230 235 240  
Thr Asp Ser Gly Tyr Gly Gly Asp Ser Glu Lys Gly Asp Leu Arg Ser  
245 250 255

Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly  
                   260                  265                  270  
 Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys  
                   275                  280                  285  
 Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser  
                   290                  295                  300  
 Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro  
 305                  310                  315                  320  
 Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu  
                   325                  330                  335  
 Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr  
                   340                  345                  350  
 Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro  
                   355                  360                  365  
 Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro  
                   370                  375                  380  
 Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu  
 385                  390                  395                  400  
 Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp  
                   405                  410

&lt;210&gt; 17

&lt;211&gt; 3817

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (164).. (2665)

&lt;400&gt; 17

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tctcgctttc alctagcgct gcactcaatg gaggggcggg caccgcagig cttaatgctg 120

tccttaaciag tgtaggaaaa cggctcaacc caccgctgcc gaa atg aag tat aag 175

Met Lys Tyr Lys

1

aat ctt atg gca agg gcc tta tat gac aat gtc cca gag tgt gcc gag 223

Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro Glu Cys Ala Glu

5 10 15 20

gaa ctg gcc ttt cgc aag gga gac atc ctg acc gtc ata gag cag aac 271

Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val Ile Glu Gln Asn

25 30 35

aca ggg gga ctg gaa gga tgg tgg ctg tgc tgc tta cac ggt cgg caa 319

Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu His Gly Arg Gln

40 45 50

ggc att gtc cca ggc aac cgg gtg aag ctt ctg att ggt ccc atg cag 367

Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile Gly Pro Met Gln

55 60 65

gag act gcc tcc agt cac gag cag cct gcc tct gga ctg atg cag cag 415

Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly Leu Met Gln Gln

70 75 80

acc ttt ggc caa cag aag ctc tat caa gtg cca aac cca cag gct gct 463

Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn Pro Gln Ala Ala

85 90 95 100

ccc cga gac acc atc tac caa gtg cca cct tcc tac caa aat cag gga 511

Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr Gln Asn Gln Gly  
105 110 115  
att tac caa gtc ccc act ggc cac ggc acc caa gaa caa gag gta tat 559  
Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu Gln Glu Val Tyr  
120 125 130  
cag gtg cca cca tca gtg cag aga agc att ggg gga acc agt ggg ccc 607  
Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly Thr Ser Gly Pro  
135 140 145  
cac gtg ggt aaa aag gtg ata acc ccc gtg agg aca ggc cat ggc tac 655  
His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr Gly His Gly Tyr  
150 155 160  
gta tac gag tac cca tcc aga tac caa aag gat gtc tat gat atc cct 703  
Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val Tyr Asp Ile Pro  
165 170 175 180  
cct tct cat acc act caa ggg gta tac gac atc cct ccc tca tca gca 751  
Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro Pro Ser Ser Ala  
185 190 195  
aaa ggc cct gtg ttt tca gtt cca gtg gga gag ata aaa cct caa ggg 799  
Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile Lys Pro Gln Gly  
200 205 210  
gtg tat gac atc ccg cct aca aaa ggg gta tat gcc att ccg ccc tct 847  
Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala Ile Pro Pro Ser  
215 220 225  
gct tgc cgg gat gaa gca ggg cit agg gaa aaa gac tat gac ttc ccc 895  
Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp Tyr Asp Phe Pro  
230 235 240  
cct ccc atg aga caa gct gga agg ccg gac ctc aga ccg gag ggg gtt 943



Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg Pro Glu Gly Val  
 245 250 255 260  
 tat gac att cct cca acc tgc acc aag cca gca ggg aag gac ctt cat 991  
 Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly Lys Asp Leu His  
 265 270 275  
 gta aaa tac aac tgt gac att cca gga gct gca gaa ccg gtg gct cga 1039  
 Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu Pro Val Ala Arg  
 280 285 290  
 agg cac cag agc ctg tcc ccg aat cac cca ccc ccg caa ctc gga cag 1087  
 Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro Gln Leu Gly Gln  
 295 300 305  
 tca gtg ggc tct cag aac gac gca tat gat gtc ccc cga ggc gtt cag 1135  
 Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro Arg Gly Val Gln  
 310 315 320  
 ttt ctt gag cca cca gca gaa acc agt gag aaa gca aac ccc cag gaa 1183  
 Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala Asn Pro Gln Glu  
 325 330 335 340  
 agg gat ggt gtt tat gat gtc cct ctg cat aac ccg cca gat gct aaa 1231  
 Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro Pro Asp Ala Lys  
 345 350 355  
 ggc tct cgg gac ttg gtg gat ggg atc aac cga ttg tct ttc tcc agt 1279  
 Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu Ser Phe Ser Ser  
 360 365 370  
 aca ggc agc acc cgg agt aac atg tcc acg tct tcc acc tcc tcc aag 1327  
 Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser Thr Ser Ser Lys  
 375 380 385

gag tcc tca ctg tca gcc tcc cca gct cag gac aaa agg ctc ttc ctg 1375  
Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys Arg Leu Phe Leu  
390 395 400  
gat cca gac aca gct att gag aga ctt cag cgg ctc cag cag gcc ctt 1423  
Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu Gln Gln Ala Leu  
405 410 415 420  
gag atg ggt gtc tcc agc cta atg gca ctg gtc act acc gac tgg cgg 1471  
Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr Thr Asp Trp Arg  
425 430 435  
tgt tac gga tat atg gaa aga cac atc aat gaa ata cgc aca gca gtg 1519  
Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile Arg Thr Ala Val  
440 445 450  
gac aag gtg gag ctg ttc ctg aag gag tac ctc cac ttt gtc aag gga 1567  
Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His Phe Val Lys Gly  
455 460 465  
gct gtt gca aat gct gcc tgc ctc ccg gaa ctc atc ctc cac aac aag 1615  
Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile Leu His Asn Lys  
470 475 480  
atg aag cgg gag ctg caa cga gtc gaa gac tcc cac cag atc ctg agt 1663  
Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His Gln Ile Leu Ser  
485 490 495 500  
caa acc agc cat gac tta aat gag tgc agc tgg tcc ctg aat atc ttg 1711  
Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser Leu Asn Ile Leu  
505 510 515  
gcc atc aac aag ccc cag aac aag tgt gac gat ctg gac cgg ttt gtg 1759  
Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu Asp Arg Phe Val  
520 525 530

atg glg gca aag acg gtg ccc gat gac gcc aag cag ctc acc aca acc 1807  
 Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln Leu Thr Thr Thr  
 535 540 545  
 atc aac acc aac gca gag gcc ctc ttc aga ccc ggc cct ggc agc ttg 1855  
 Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly Pro Gly Ser Leu  
 550 555 560  
 cat ctg aag aat ggg ccg gag agc atc atg aac tca acg gag tac cca 1903  
 His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser Thr Glu Tyr Pro  
 565 570 575 580  
 cac ggt ggc tcc cag gga cag ctg ctg cat cct ggt gac cac aag gcc 1951  
 His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly Asp His Lys Ala  
 585 590 595  
 cag gcc cac aac aag gca ctg ccc cca ggc ctg agc aag gag cag gcc 1999  
 Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser Lys Glu Gln Ala  
 600 605 610  
 cct gac tgt agc agc agt gat ggt tct gag agg agc tgg atg gat gac 2047  
 Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser Trp Met Asp Asp  
 615 620 625  
 tac gat tac gtc cac cta cag ggt aag gag gag ttt gag agg caa cag 2095  
 Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe Glu Arg Gln Gln  
 630 635 640  
 aaa gag cta ttg gaa aaa gag aat atc atg aaa cag aac aag atg cag 2143  
 Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln Asn Lys Met Gln  
 645 650 655 660  
 ctg gaa cat cat cag ctg agc cag ttc cag ctg ttg gaa caa gag att 2191  
 Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu Glu Gln Glu Ile

665	670	675	
aca aag ccc gtg gag aat gac atc tgc aag tgg aag ccc tct cag agc	2239		
Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys Pro Ser Gln Ser			
680	685	690	
cta ccc acc aca aac agt ggc gtg agt gct cag gat cgg cag ttg ctg	2287		
Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp Arg Gln Leu Leu			
695	700	705	
tgc ttc tac tai gac caa tgt gag acc cat ttc att tcc ctt ctc aac	2335		
Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile Ser Leu Leu Asn			
710	715	720	
gcc att gac gca ctc ttc agt tgt gtc agc tca gcc cag ccc ccg cga	2383		
Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala Gln Pro Pro Arg			
725	730	735	740
atc ttc gtg gca cac agc aag ttt gtc atc ctc agt gca cac aaa ctg	2431		
Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser Ala His Lys Leu			
745	750	755	
gtg ttc att gga gac acg ctg aca cgg cag gtg act gcc cag gac att	2479		
Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr Ala Gln Asp Ile			
760	765	770	
cgc aac aaa gtc atg aac tcc agc aac cag ctc tgc gag cag ctc aag	2527		
Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys Glu Gln Leu Lys			
775	780	785	
act ata gtc atg gca acc aag atg gcc gcc ctc cat tac ccc agc acc	2575		
Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His Tyr Pro Ser Thr			
790	795	800	
acg gcc ctg cag gaa atg gtg cac caa gtg aca gac ctt tct aga aat	2623		
Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp Leu Ser Arg Asn			

805	810	815	820	
gcc cag ctg ttc aag cgc tct ttg ctg gag atg gca acg ttc				2665
Ala Gln Leu Phe Lys Arg Ser Leu Leu Glu Met Ala Thr Phe				
825	830			
tgagaagaaa aaaaagagga aggggactgc gttacgggt actaaggaaa actggaaata				2725
ctgtctgggt ttgtaaatg ttatctatit ttgtagataa ttttataata aatgaaata				2785
ttttaacatt ttatgggtca gacaacttgc agaaattcag ggagctggag agggaaaact				2845
ttttttcccc cctgagtggt ctatgtata cacagaagta tctgagacat aaactgtaca				2905
gaaaacttgt ccacgtcctt ttgtatgccc atgtattcat gtttttgitt gtagatgitt				2965
gtctgatgca ttctattaaa aaaaaaacca tgaattacga agcaccttag taagcacctt				3025
ctaatgctgc attttttttg ttgtttgtta aaacalccag ctggttataa tattgttctc				3085
cacgtccttg tgaatgattc gagcctggca ctgggaatct gggaagcata gtttatttgc				3145
aagitttcac ctccaaatc atgaggcata gcatgactta ttcttgtttt gaaaactcct				3205
ttcaaaactg accatcttaa acacatgatg gccaaagtgc acaaagccct ctgctggaga				3265
catttacgaa tatatatgtg gatccaagtc tcatagttta ggctgtggag ggaagagaga				3325
ccagagagtt tagaggccag gaccacagtt aggattgggt tgtttcaata ctgagagaca				3385
gtacaataa aaggagagca attgcctccc tggggctggt caatcttctg cttttgtgag				3445
tggttcagtc atgaggtttt ccaaaagatg tttttagagt tgtaaaaacc atatttgcag				3505
caaagattta caaaggcgtc tcagactatg attgttcacc aaaatagggg aatgggttga				3565
tccgccagtt gcaagtagag gcctttctga ctcttaatat tcactttggt gctactacct				3625
ccattacctg aggaactggc caggctcctg atcatggaac tatagagcta ccagacatat				3685
cctgctctct aagggaatit attgctatct tgcaccttct ttaaaactca aaaaacatat				3745
gcagacctga cactcaagag tggctagcta cacagagtc atctaatttt tgcaacttcc				3805
ccccccgaat tc				3817

<210> 18

<211> 834

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

Met Lys Tyr Lys Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro  
1 5 10 15  
Glu Cys Ala Glu Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val  
20 25 30  
Ile Glu Gln Asn Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu  
35 40 45  
His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile  
50 55 60  
Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly  
65 70 75 80  
Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn  
85 90 95  
Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr  
100 105 110  
Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu  
115 120 125  
Gln Glu Val Tyr Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly  
130 135 140  
Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr  
145 150 155 160  
Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val  
165 170 175  
Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro

180	185	190	
Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile			
195	200	205	
Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala			
210	215	220	
Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp			
225	230	235	240
Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg			
245	250	255	
Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly			
260	265	270	
Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu			
275	280	285	
Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro			
290	295	300	
Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro			
305	310	315	320
Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala			
325	330	335	
Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro			
340	345	350	
Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu			
355	360	365	
Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser			
370	375	380	
Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys			
385	390	395	400

Arg Leu Phe Leu Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu			
405	410	415	
Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr			
420	425	430	
Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile			
435	440	445	
Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His			
450	455	460	
Phe Val Lys Gly Ala Val Ala Asn Ala Ala Cys Leu Pro Glu Leu Ile			
465	470	475	480
Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His			
485	490	495	
Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser			
500	505	510	
Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu			
515	520	525	
Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln			
530	535	540	
Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly			
545	550	555	560
Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser			
565	570	575	
Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly			
580	585	590	
Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser			
595	600	605	



Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser  
 610 615 620  
 Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe  
 625 630 635 640  
 Glu Arg Gln Gln Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln  
 645 650 655  
 Asn Lys Met Gln Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu  
 660 665 670  
 Glu Gln Glu Ile Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys  
 675 680 685  
 Pro Ser Gln Ser Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp  
 690 695 700  
 Arg Gln Leu Leu Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile  
 705 710 715 720  
 Ser Leu Leu Asn Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala  
 725 730 735  
 Gln Pro Pro Arg Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser  
 740 745 750  
 Ala His Lys Leu Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr  
 755 760 765  
 Ala Gln Asp Ile Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys  
 770 775 780  
 Glu Gln Leu Lys Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His  
 785 790 795 800  
 Tyr Pro Ser Thr Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp  
 805 810 815  
 Leu Ser Arg Asn Ala Gln Leu Phe Lys Arg Ser Leu Leu Glu Met Ala

820 825 830

Thr Phe

<210> 19

<211> 567

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36).. (506)

<400> 19

tgtgacgcct gcagggctgg gacctgacgg tgaag atg ctg gcg ggc aac gaa 53

Met Leu Ala Gly Asn Glu

1 5

ttc cag gtg tcc ctg agc agc tcc atg tgc gtg tca gag ctg aag gcg 101

Phe Gln Val Ser Leu Ser Ser Ser Met Ser Val Ser Glu Leu Lys Ala

10 15 20

cag atc acc cag aac att ggc gtg cac gcc ttc cag cag cgt ctg gct 149

Gln Ile Thr Gln Asn Ile Gly Val His Ala Phe Gln Gln Arg Leu Ala

25 30 35

gtc cac ccg agc ggt gtg gcg ctg cag gac agg gtc ccc ctt gcc agc 197

Val His Pro Ser Gly Val Ala Leu Gln Asp Arg Val Pro Leu Ala Ser

40 45 50

cag ggc ctg ggc cct ggc agc acg gtc ctg ctg gtg gtg gac aaa tgc 245

Gln Gly Leu Gly Pro Gly Ser Thr Val Leu Leu Val Val Asp Lys Cys

55 60 65 70

gac gaa cct ctg agc atc ctg gtg agg aat aac aag ggc cgc agc agc 293

Asp Glu Pro Leu Ser Ile Leu Val Arg Asn Asn Lys Gly Arg Ser Ser  
                     75                    80                    85  
 acc tac gag gtg cgg ctg acg cag acc gig gcc cac ctg aag cag caa 341  
 Thr Tyr Glu Val Arg Leu Thr Gln Thr Val Ala His Leu Lys Gln Gln  
                     90                    95                    100  
 gtg agc ggg ctg gag ggt gtg cag gac gac ctg ttc tgg ctg acc ttc 389  
 Val Ser Gly Leu Glu Gly Val Gln Asp Asp Leu Phe Trp Leu Thr Phe  
                     105                    110                    115  
 gag ggg aag ccc ctg gag gac cag ctc ccg ctg ggg gag tac ggc ctc 437  
 Glu Gly Lys Pro Leu Glu Asp Gln Leu Pro Leu Gly Glu Tyr Gly Leu  
                     120                    125                    130  
 aag ccc ctg agc acc glg ttc atg aat ctg cgc ctg cgg gga ggc ggc 485  
 Lys Pro Leu Ser Thr Val Phe Met Asn Leu Arg Leu Arg Gly Gly Gly  
                     135                    140                    145                    150  
 aca gag cct ggc ggg cgg agc taagggcctc caccagcctc cgagcaggat 536  
 Thr Glu Pro Gly Gly Arg Ser  
                     155  
 caagggccgg aataaaggct gtgtgaagag a 567

&lt;210&gt; 20

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

Met Leu Ala Gly Asn Glu Phe Gln Val Ser Leu Ser Ser Ser Met Ser  
           1                    5                    10                    15  
 Val Ser Glu Leu Lys Ala Gln Ile Thr Gln Asn Ile Gly Val His Ala

20 25 30  
 Phe Gln Gln Arg Leu Ala Val His Pro Ser Gly Val Ala Leu Gln Asp  
 35 40 45  
 Arg Val Pro Leu Ala Ser Gln Gly Leu Gly Pro Gly Ser Thr Val Leu  
 50 55 60  
 Leu Val Val Asp Lys Cys Asp Glu Pro Leu Ser Ile Leu Val Arg Asn  
 65 70 75 80  
 Asn Lys Gly Arg Ser Ser Thr Tyr Glu Val Arg Leu Thr Gln Thr Val  
 85 90 95  
 Ala His Leu Lys Gln Gln Val Ser Gly Leu Glu Gly Val Gln Asp Asp  
 100 105 110  
 Leu Phe Trp Leu Thr Phe Glu Gly Lys Pro Leu Glu Asp Gln Leu Pro  
 115 120 125  
 Leu Gly Glu Tyr Gly Leu Lys Pro Leu Ser Thr Val Phe Met Asn Leu  
 130 135 140  
 Arg Leu Arg Gly Gly Gly Thr Glu Pro Gly Gly Arg Ser  
 145 150 155

&lt;210&gt; 21

&lt;211&gt; 5095

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (14).. (2593)

&lt;400&gt; 21

agaggctgcg agc atg ggg ccc tgg ggc tgg aaa ttg cgc tgg acc gtc 49

Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val																
1		5		10												
gcc	ttg	ctc	ctc	gcc	gcg	gcg	ggg	act	gca	gtg	ggc	gac	aga	tgt	gaa	97
Ala Leu Leu Leu Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu																
15		20		25												
aga	aac	gag	ttc	cag	tgc	caa	gac	ggg	aaa	tgc	atc	tcc	tac	aag	tgg	145
Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp																
30		35		40												
gtc	tgc	gat	ggc	agc	gct	gag	tgc	cag	gat	ggc	tct	gat	gag	tcc	cag	193
Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln																
45		50		55		60										
gag	acg	tgc	ttg	tct	gtc	acc	tgc	aaa	tcc	ggg	gac	ttc	agc	tgt	ggg	241
Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly																
65		70		75												
ggc	cgt	gtc	aac	cgc	tgc	att	cct	cag	ttc	tgg	agg	tgc	gat	ggc	caa	289
Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln																
80		85		90												
gtg	gac	tgc	gac	aac	ggc	tca	gac	gag	caa	ggc	tgt	ccc	ccc	aag	acg	337
Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr																
95		100		105												
tgc	tcc	cag	gac	gag	ttt	cgc	tgc	cac	gat	ggg	aag	tgc	atc	tct	cgg	385
Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg																
110		115		120												
cag	ttc	gtc	tgt	gac	tca	gac	cgg	gac	tgc	ttg	gac	ggc	tca	gac	gag	433
Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu																
125		130		135		140										

gcc tcc tgc ccg glg ctc acc tgt ggt ccc gcc agc ttc cag tgc aac 481  
 Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn  
 145 150 155  
 agc tcc acc tgc atc ccc cag cgg tgg gcc tgc gac aac gac ccc gac 529  
 Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp  
 160 165 170  
 tgc gaa gat ggc tgc gat gag tgg ccg cag cgc tgt agg ggt ctt tac 577  
 Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr  
 175 180 185  
 glg ttc caa ggg gac agt agc ccc tgc tgc gcc ttc gag ttc cac tgc 625  
 Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys  
 190 195 200  
 cta agt ggc gag tgc atc cac tcc agc tgg cgc tgt gat ggt ggc ccc 673  
 Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro  
 205 210 215 220  
 gac tgc aag gac aaa tct gac gag gaa aac tgc gct gtg gcc acc tgt 721  
 Asp Cys Lys Asp Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys  
 225 230 235  
 cgc cct gac gaa ttc cag tgc tct gat gga aac tgc atc cat ggc agc 769  
 Arg Pro Asp Glu Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser  
 240 245 250  
 cgg cag tgt gac cgg gaa tat gac tgc aag gac atg agc gat gaa gtt 817  
 Arg Gln Cys Asp Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val  
 255 260 265  
 ggc tgc gtt aat gtg aca ctc tgc gag gga ccc aac aag ttc aag tgt 865  
 Gly Cys Val Asn Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys  
 270 275 280

cac agc ggc gaa tgc atc acc ctg gac aaa gtc tgc aac atg gct aga 913  
 His Ser Gly Glu Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg  
 285 290 295 300  
 gac tgc cgg gac tgg tca gat gaa ccc atc aaa gag tgc ggg acc aac 961  
 Asp Cys Arg Asp Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn  
 305 310 315  
 gaa tgc ttg gac aac aac ggc ggc tgt tcc cac gtc tgc aat gac ctt 1009  
 Glu Cys Leu Asp Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu  
 320 325 330  
 aag atc ggc tac gag tgc ctg tgc ccc gac ggc ttc cag ctg gtg gcc 1057  
 Lys Ile Gly Tyr Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala  
 335 340 345  
 cag cga aga tgc gaa gat atc gat gag tgt cag gat ccc gac acc tgc 1105  
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 Ser Gln Leu Cys Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu  
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 Glu Gly Phe Gln Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly  
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 Ser Ile Ala Tyr Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met  
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 Thr Leu Asp Arg Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn

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Val Val Ala Leu Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser  
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Gly Val Ser Ser Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro  
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Asp Pro Val His Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala  
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Gly Arg Leu Tyr Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile			
575	580	585	
gat gtc aat ggg ggc aac cgg aag acc atc ttg gag gat gaa aag agg	1825		
Asp Val Asn Gly Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg			
590	595	600	
ctg gcc cac ccc ttc tcc ttg gcc gtc ttt gag gac aaa gta ttt tgg	1873		
Leu Ala His Pro Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp			
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aca gat atc atc aac gaa gcc att ttc agt gcc aac cgc ctc aca ggt	1921		
Thr Asp Ile Ile Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly			
625	630	635	
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640	645	650	
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Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu			
655	660	665	
agg acc acc ctg agc aat ggc ggc tgc cag tat ctg tgc ctc cct gcc	2065		
Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala			
670	675	680	
ccg cag atc aac ccc cac tcg ccc aag ttt acc tgc gcc tgc ccg gac	2113		
Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp			
685	690	695	700
ggc atg ctg ctg gcc agg gac atg agg agc tgc ctc aca gag gct gag	2161		

Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu  
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 gct gca glg gcc acc cag gag aca tcc acc glc agg cta aag gtc agc 2209  
 Ala Ala Val Ala Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser  
 720 725 730  
 tcc aca gcc gta agg aca cag cac aca acc acc cgg cct gtt ccc gac 2257  
 Ser Thr Ala Val Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp  
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 cag aag acc aca gag gat gag gtc cac att tgc cac aac cag gac ggc 2545  
 Gln Lys Thr Thr Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly  
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Tyr Ser Tyr Pro Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala

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<211> 860

<212> PRT

<213> Homo sapiens

<400> 22

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 Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu  
 50 55 60  
 Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn  
 65 70 75 80  
 Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp  
 85 90 95  
 Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp  
 100 105 110  
 Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys  
 115 120 125  
 Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro  
 130 135 140  
 Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys  
 145 150 155 160  
 Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly  
 165 170 175  
 Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly  
 180 185 190  
 Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu  
 195 200 205  
 Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp  
 210 215 220  
 Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu  
 225 230 235 240

Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser Arg Gln Cys Asp  
 245 250 255  
 Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val Gly Cys Val Asn  
 260 265 270  
 Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu  
 275 280 285  
 Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp  
 290 295 300  
 Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp  
 305 310 315 320  
 Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr  
 325 330 335  
 Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala Gln Arg Arg Cys  
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 Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys Ser Gln Leu Cys  
 355 360 365  
 Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu Glu Gly Phe Gln  
 370 375 380  
 Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Gly Ser Ile Ala Tyr  
 385 390 395 400  
 Leu Phe Phe Thr Asn Arg His Glu Val Arg Lys Met Thr Leu Asp Arg  
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 Ser Glu Tyr Thr Ser Leu Ile Pro Asn Leu Arg Asn Val Val Ala Leu  
 420 425 430  
 Asp Thr Glu Val Ala Ser Asn Arg Ile Tyr Trp Ser Asp Leu Ser Gln  
 435 440 445

Arg Met Ile Cys Ser Thr Gln Leu Asp Arg Ala His Gly Val Ser Ser  
450 455 460  
Tyr Asp Thr Val Ile Ser Arg Asp Ile Gln Ala Pro Asp Gly Leu Ala  
465 470 475 480  
Val Asp Trp Ile His Ser Asn Ile Tyr Trp Thr Asp Ser Val Leu Gly  
485 490 495  
Thr Val Ser Val Ala Asp Thr Lys Gly Val Lys Arg Lys Thr Leu Phe  
500 505 510  
Arg Glu Asn Gly Ser Lys Pro Arg Ala Ile Val Val Asp Pro Val His  
515 520 525  
Gly Phe Met Tyr Trp Thr Asp Trp Gly Thr Pro Ala Lys Ile Lys Lys  
530 535 540  
Gly Gly Leu Asn Gly Val Asp Ile Tyr Ser Leu Val Thr Glu Asn Ile  
545 550 555 560  
Gln Trp Pro Asn Gly Ile Thr Leu Asp Leu Leu Ser Gly Arg Leu Tyr  
565 570 575  
Trp Val Asp Ser Lys Leu His Ser Ile Ser Ser Ile Asp Val Asn Gly  
580 585 590  
Gly Asn Arg Lys Thr Ile Leu Glu Asp Glu Lys Arg Leu Ala His Pro  
595 600 605  
Phe Ser Leu Ala Val Phe Glu Asp Lys Val Phe Trp Thr Asp Ile Ile  
610 615 620  
Asn Glu Ala Ile Phe Ser Ala Asn Arg Leu Thr Gly Ser Asp Val Asn  
625 630 635 640  
Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met Val Leu Phe His  
645 650 655  
Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu Arg Thr Thr Leu

660                      665                      670  
 Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala Pro Gln Ile Asn  
 675                      680                      685  
 Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp Gly Met Leu Leu  
 690                      695                      700  
 Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu Ala Ala Val Ala  
 705                      710                      715                      720  
 Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Ser Ser Thr Ala Val  
 725                      730                      735  
 Arg Thr Gln His Thr Thr Thr Arg Pro Val Pro Asp Thr Ser Arg Leu  
 740                      745                      750  
 Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser  
 755                      760                      765  
 His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro  
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 Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val  
 785                      790                      795                      800  
 Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys  
 805                      810                      815  
 Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr  
 820                      825                      830  
 Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser Tyr Pro  
 835                      840                      845  
 Ser Arg Gln Met Val Ser Leu Glu Asp Asp Val Ala  
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&lt;211&gt; 1660

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (50).. (529)

&lt;400&gt; 23

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Met Leu Leu

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ctg ttg ctg agt atc atc gtc ctc cac gtc gcg gtg ctg gtg ctg ctg 106

Leu Leu Leu Ser Ile Ile Val Leu His Val Ala Val Leu Val Leu Leu

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10

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ttc gtc tcc acg atc gtc agc caa tgg atc gtg ggc aat gga cac gca 154

Phe Val Ser Thr Ile Val Ser Gln Trp Ile Val Gly Asn Gly His Ala

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25

30

35

act gat ctc tgg cag aac tgt agc acc tct tcc tca gga aat gtc cac 202

Thr Asp Leu Trp Gln Asn Cys Ser Thr Ser Ser Ser Gly Asn Val His

40

45

50

cac tgt ttc tca tca tca cca aac gaa tgg ctg cag tct gtc cag gcc 250

His Cys Phe Ser Ser Ser Pro Asn Glu Trp Leu Gln Ser Val Gln Ala

55

60

65

acc atg atc ctg tcg atc atc ttc agc att ctg tct ctg ttc ctg ttc 298

Thr Met Ile Leu Ser Ile Ile Phe Ser Ile Leu Ser Leu Phe Leu Phe

70

75

80

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Phe Cys Gln Leu Phe Thr Leu Thr Lys Gly Gly Arg Phe Tyr Ile Thr  
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 gga atc ttc caa att ctt gct ggt ctg tgc gtg atg agt gct gcg gcc 394  
 Gly Ile Phe Gln Ile Leu Ala Gly Leu Cys Val Met Ser Ala Ala Ala  
 100 105 110 115  
 atc tac acg gtg agg cac ccg gag tgg cat ctc acc tcg gat tac tcc 442  
 Ile Tyr Thr Val Arg His Pro Glu Trp His Leu Thr Ser Asp Tyr Ser  
 120 125 130  
 tac ggt ttc gcc tac atc ctg gcc tgg gtg gcc ttc ccc ctg gcc ctt 490  
 Tyr Gly Phe Ala Tyr Ile Leu Ala Trp Val Ala Phe Pro Leu Ala Leu  
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 Leu Ser Gly Val Ile Tyr Val Ile Leu Arg Lys Arg Glu  
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<211> 160

<212> PRT

<213> Homo sapiens

<400> 24

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Gly His Ala Thr Asp Leu Trp Gln Asn Cys Ser Thr Ser Ser Ser Gly

35 40 45

Asn Val His His Cys Phe Ser Ser Ser Pro Asn Glu Trp Leu Gln Ser

50 55 60

Val Gln Ala Thr Met Ile Leu Ser Ile Ile Phe Ser Ile Leu Ser Leu

65 70 75 80

Phe Leu Phe Phe Cys Gln Leu Phe Thr Leu Thr Lys Gly Gly Arg Phe

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Tyr Ile Thr Gly Ile Phe Gln Ile Leu Ala Gly Leu Cys Val Met Ser

100 105 110

Ala Ala Ala Ile Tyr Thr Val Arg His Pro Glu Trp His Leu Thr Ser

115                      120                      125  
 Asp Tyr Ser Tyr Gly Phe Ala Tyr Ile Leu Ala Trp Val Ala Phe Pro  
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<220>

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Met Ala Trp Arg Cys Pro

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agg atg ggc agg gtc ccg ctg gcc tgg tgc ttg gcg ctg tgc ggc tgg 101

Arg Met Gly Arg Val Pro Leu Ala Trp Cys Leu Ala Leu Cys Gly Trp

10

15

20

gcg tgc atg gcc ccc agg ggc acg cag gct gaa gaa agt ccc ttc gtg 149

Ala Cys Met Ala Pro Arg Gly Thr Gln Ala Glu Glu Ser Pro Phe Val

25

30

35

ggc aac cca ggg aat atc aca ggt gcc cgg gga ctc acg ggc acc ctt 197

Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg Gly Leu Thr Gly Thr Leu

40

45

50

cgg tgt cag ctc cag gtt cag gga gag ccc ccc gag gta cat tgg ctt 245

Arg Cys Gln Leu Gln Val Gln Gly Glu Pro Pro Glu Val His Trp Leu  
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 Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp Ser Thr Gln Thr Gln Val  
 75 80 85  
 ccc ctg ggt gag gat gaa cag gat gac tgg ata gtg gtc agc cag ctc 341  
 Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp Ile Val Val Ser Gln Leu  
 90 95 100  
 aga atc acc tcc ctg cag ctt tcc gac acg gga cag tac cag tgt ttg 389  
 Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr Gly Gln Tyr Gln Cys Leu  
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 gtg ttt ctg gga cat cag acc ttc gtg tcc cag cct ggc tat gtt ggg 437  
 Val Phe Leu Gly His Gln Thr Phe Val Ser Gln Pro Gly Tyr Val Gly  
 120 125 130  
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 Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu Pro Glu Asp Arg Thr Val  
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 gag ccc gtg gac cta ctc tgg ctc cag gat gct gtc ccc ctg gcc acg 581  
 Glu Pro Val Asp Leu Leu Trp Leu Gln Asp Ala Val Pro Leu Ala Thr  
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 gct cca ggt cac ggc ccc cag cgc agc ctg cat gtt cca ggg ctg aac 629  
 Ala Pro Gly His Gly Pro Gln Arg Ser Leu His Val Pro Gly Leu Asn  
 185 190 195

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Lys Thr Ser Ser Phe Ser Cys Glu Ala His Asn Ala Lys Gly Val Thr  
200 205 210  
aca tcc cgc aca gcc acc atc aca gtg ctc ccc cag cag ccc cgt aac 725  
Thr Ser Arg Thr Ala Thr Ile Thr Val Leu Pro Gln Gln Pro Arg Asn  
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Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr His Cys Thr Leu Gln Ala  
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Val Leu Ser Asp Asp Gly Met Gly Ile Gln Ala Gly Glu Pro Asp Pro  
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Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser Val Pro Pro His Gln Leu  
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Arg Leu Gly Ser Leu His Pro His Pro Pro Tyr His Ile Arg Val Ala  
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Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp Thr His Trp Leu Pro Val  
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Glu Thr Pro Glu Gly Val Pro Leu Gly Pro Pro Glu Asn Ile Ser Ala  
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Pro	Thr	Val	Glu	Arg	Gly	Glu	Leu	Val	Val	Arg	Tyr	Arg	Val	Arg	Lys	
490	495	500														
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Ser	Tyr	Ser	Arg	Arg	Thr	Thr	Glu	Ala	Thr	Leu	Asn	Ser	Leu	Gly	Ile	
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Lys	Val	Ala	Leu	Gly	Lys	Thr	Leu	Gly	Glu	Gly	Glu	Phe	Gly	Ala	Val	
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Met	Glu	Gly	Gln	Leu	Asn	Gln	Asp	Asp	Ser	Ile	Leu	Lys	Val	Ala	Val	
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Lys	Thr	Met	Lys	Ile	Ala	Ile	Cys	Thr	Arg	Ser	Glu	Leu	Glu	Asp	Phe	
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ctg	agt	gaa	gcg	gtc	tgc	atg	aag	gaa	ttt	gac	cat	ccc	aac	gtc	atg	1829
Leu	Ser	Glu	Ala	Val	Cys	Met	Lys	Glu	Phe	Asp	His	Pro	Asn	Val	Met	
585	590	595														
agg	ctc	atc	ggt	gtc	tgt	ttc	cag	ggt	tct	gaa	cga	gag	agc	ttc	cca	1877
Arg	Leu	Ile	Gly	Val	Cys	Phe	Gln	Gly	Ser	Glu	Arg	Glu	Ser	Phe	Pro	
600	605	610														
gca	cct	gtg	gtc	atc	tta	cct	ttc	atg	aaa	cat	gga	gac	cta	cac	agc	1925
Ala	Pro	Val	Val	Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	Leu	His	Ser	



615	620	625	630	
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Phe Leu Leu Tyr Ser Arg Leu Gly Gly Gln Pro Val Tyr Leu Pro Thr				
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cag atg cta glg aag ttc atg gca gac atc gcc agt ggc atg gag tat	2021			
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Met Leu Asn Glu Asn Met Ser Val Cys Val Ala Asp Phe Gly Leu Ser				
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Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys				
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atg cca gtc aag tgg att gcc att gag agt cta gct gac cgt gtc tac	2213			
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715	720	725		
acc agc aag agc gat gtg tgg tcc ttc ggg gtg aca atg tgg gag att	2261			
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gcc aca aga ggc caa acc cca tat ccg ggc gtg gag aac agc gag att	2309			
Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile				
745	750	755		
tat gac tat ctg cgc cag gga aat cgc ctg aag cag cct gcg gac tgt	2357			

Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys  
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 Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg Cys Trp Glu Leu Asn Pro  
 775 780 785 790  
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 Ala Pro Gly Gln Glu Asp Gly Ala  
 890  
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 ggccctaaaa 3116

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<211> 894

<212> PRT

<213> Homo sapiens

<400> 26

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Leu Ala Leu Cys Gly Trp Ala Cys Met Ala Pro Arg Gly Thr Gln Ala

20 25 30

Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg

35 40 45

Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro

50 55 60

Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp

65 70 75 80

Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp

85 90 95

Ile Val Val Ser Gln Leu Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr

100 105 110

Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser

115                      120                      125  
 Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu  
 130                      135                      140  
 Pro Glu Asp Arg Thr Val Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys  
 145                      150                      155                      160  
 Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp  
 165                      170                      175  
 Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu  
 180                      185                      190  
 His Val Pro Gly Leu Asn Lys Thr Ser Ser Phe Ser Cys Glu Ala His  
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 Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu  
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 Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu  
 225                      230                      235                      240  
 Leu Glu Val Ala Trp Thr Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr  
 245                      250                      255  
 His Cys Thr Leu Gln Ala Val Leu Ser Asp Asp Gly Met Gly Ile Gln  
 260                      265                      270  
 Ala Gly Glu Pro Asp Pro Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser  
 275                      280                      285  
 Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Pro Pro  
 290                      295                      300  
 Tyr His Ile Arg Val Ala Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp  
 305                      310                      315                      320  
 Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro

325 330 335  
Pro Glu Asn Ile Ser Ala Thr Arg Asn Gly Ser Gln Ala Phe Val His  
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Trp Gln Glu Pro Arg Ala Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg  
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Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly  
370 375 380  
Leu Arg Gln Glu Val Thr Leu Glu Leu Gln Gly Asp Gly Ser Val Ser  
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Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro  
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Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Gly Glu Ala Gln  
420 425 430  
Pro Val His Gln Leu Val Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp  
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Pro Trp Trp Tyr Val Leu Leu Gly Ala Val Val Ala Ala Ala Cys Val  
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Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly Glu Leu Val Val  
485 490 495  
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Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp  
515 520 525  
Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys Thr Leu Gly Glu  
530 535 540

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545 550 555 560  
Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala Ile Cys Thr Arg  
565 570 575  
Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys Met Lys Glu Phe  
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595 600 605  
Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu Pro Phe Met Lys  
610 615 620  
His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg Leu Gly Gly Gln  
625 630 635 640  
Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe Met Ala Asp Ile  
645 650 655  
Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe Ile His Arg Asp  
660 665 670  
Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val  
675 680 685  
Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg  
690 695 700  
Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser  
705 710 715 720  
Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe Gly  
725 730 735  
Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly  
740 745 750

Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu  
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Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg  
770 775 780  
Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg  
785 790 795 800  
Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro  
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820 825 830  
Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro  
835 840 845  
Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val His Pro Ala Gly  
850 855 860  
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&lt;211&gt; 3781

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&lt;220&gt;

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&lt;222&gt; (4).. (2994)

&lt;400&gt; 27

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ttc ggc gtc aac gag agt acg ggg ctg agc ctg gaa cag gtc aag aag   96
    Phe Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys
      20             25             30
ctt aag gag aga tgg ggc tcc aac gag tta ccg gct gaa gaa gga aaa  144
    Leu Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys
      35             40             45
acc ttg ctg gaa ctt gtg att gag cag ttt gaa gac ttg cta gtt agg  192
    Thr Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg
      50             55             60
att tta tta ctg gca gca tgt ata tct ttt gtt ttg gct tgg ttt gaa  240
    Ile Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu
      65             70             75
gaa ggt gaa gaa aca att aca gcc ttt gta gaa cct ttt gta att tta  288
    Glu Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu
      80             85             90             95
ctc ata tta gta gcc aat gca att gtg ggt gta tgg cag gaa aga aat  336
    Leu Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn
      100            105            110
gct gaa aat gcc atc gaa gcc ctt aag gaa tat gag cct gaa atg ggc  384
    Ala Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly
      115            120            125
aaa gtg tat cga cag gac aga aag agt gtg cag cgg att aaa gct aaa  432
    Lys Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys
      130            135            140

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 Asp Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val  
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 Pro Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val  
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 Asp Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr  
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 Asp Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met  
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 Val Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu  
 240 245 250 255  
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Val Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu			
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gct ctt gga act cgc aga atg gca aag aaa aat gcc att gtt cga agc	1008		
Ala Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser			
320	325	330	335
ctc ccg tct gtg gaa acc ctt ggt tgt act tct gtt atc tgc tca gac	1056		
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Lys Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe			
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Lys Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr			
400	405	410	415
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Ile Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys			

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Gly Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys			
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Leu Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser			
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Val Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met			
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Phe Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile			
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Arg Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys			
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Ile Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg			
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Cys Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met  
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 Glu Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly  
                     690                      695                      700  
 gtg aac gat gct cct gct ctg aag aaa gcc gag att ggc att gct atg 2160

Val Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met  
 705 710 715  
 ggc tct ggc act gcg gtg gct aaa acc gcc tct gag atg gtc ctg gcg 2208  
 Gly Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala  
 720 725 730 735  
 gat gac aac ttc tcc acc att gtg gct gcc gtt gag gag ggg cgg gca 2256  
 Asp Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala  
 740 745 750  
 atc tac aac aac atg aaa cag ttc atc cgc tac ctc atc tcg tcc aac 2304  
 Ile Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn  
 755 760 765  
 gtc ggg gaa gtt gtc tgt att ttc ctg aca gca gcc ctt gga ttt ccc 2352  
 Val Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro  
 770 775 780  
 gag gct ttg att cct gtt cag ctg ctc tgg gtc aat ctg gtg aca gat 2400  
 Glu Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp  
 785 790 795  
 ggc ctg cct gcc act gca ctg ggg ttc aac cct cct gat ctg gac atc 2448  
 Gly Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile  
 800 805 810 815  
 atg aat aaa cct ccc cgg aac cca aag gaa cca ttg atc agc ggg tgg 2496  
 Met Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp  
 820 825 830  
 ctc ttt ttc cgt tac ttg gct att ggc tgt tac gtc ggc gct gct acc 2544  
 Leu Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr  
 835 840 845

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 Val Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg  
 850 855 860  
 gtg tcc ttc tac cag ctg agt cat ttc cta cag tgt aaa gag gac aac 2640  
 Val Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn  
 865 870 875  
 ccg gac ttt gaa ggc gtg gat tgt gca atc ttt gaa tcc cca tac ccg 2688  
 Pro Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro  
 880 885 890 895  
 atg aca atg gcg ctc tct gtt cta gta act ata gaa atg tgt aac gcc 2736  
 Met Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala  
 900 905 910  
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 915 920 925  
 gag aac atc tgg ctc gtg ggc tcc atc tgc ctg tcc atg tca ctc cac 2832  
 Glu Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His  
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 ttc ctg atc ctc tat gtc gaa ccc ttg cca ctc atc ttc cag atc aca 2880  
 Phe Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr  
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 Pro Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro  
 960 965 970 975  
 gtg att ctc atg gat gag acg ctc aag ttt gtg gcc cgc aac tac ctg 2976  
 Val Ile Leu Met Asp Glu Thr Leu Lys Phe Val Ala Arg Asn Tyr Leu  
 980 985 990

gaa cct gca ata ctg gag taaccgcttc cttaaaccatt ttgcagaaat 3024

Glu Pro Ala Ile Leu Glu

995

gtaagggigt tcggttgcgt gcatgtgcgt ttttagcaac acatctacca accctgtgca 3084

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<210> 28

<211> 997

<212> PRT

<213> Homo sapiens

<400> 28

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5

10

15

Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys Leu

20

25

30

Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys Thr

35 40 45  
 Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile  
 50 55 60  
 Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu  
 65 70 75 80  
 Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu  
 85 90 95  
 Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala  
 100 105 110  
 Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys  
 115 120 125  
 Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp  
 130 135 140  
 Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro  
 145 150 155 160  
 Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp  
 165 170 175  
 Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp  
 180 185 190  
 Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu  
 195 200 205  
 Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val  
 210 215 220  
 Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val  
 225 230 235 240  
 Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe



245 250 255  
Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp  
260 265 270  
Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp  
275 280 285  
Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val  
290 295 300  
Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala  
305 310 315 320  
Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu  
325 330 335  
Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys  
340 345 350  
Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile  
355 360 365  
Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr Ile  
370 375 380  
Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp Lys  
385 390 395 400  
Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile  
405 410 415  
Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys Gly  
420 425 430  
Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys Leu  
435 440 445  
Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser Lys  
450 455 460

Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met Lys  
 465                      470                      475                      480  
 Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val  
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 Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met Phe  
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 Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile Arg  
                     515                      520                      525  
 Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys Ile  
                     530                      535                      540  
 Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg Cys  
 545                      550                      555                      560  
 Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met His  
                     565                      570                      575  
 Leu Glu Asp Ser Ala Asn Phe Ile Lys Tyr Glu Thr Asn Leu Thr Phe  
                     580                      585                      590  
 Val Gly Cys Val Gly Met Leu Asp Pro Pro Arg Ile Glu Val Ala Ser  
                     595                      600                      605  
 Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile Thr  
                     610                      615                      620  
 Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly Ile  
 625                      630                      635                      640  
 Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg Glu  
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 Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn Ala  
                     660                      665                      670

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Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu  
 675 680 685  
 Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val  
 690 695 700  
 Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly  
 705 710 715 720  
 Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp  
 725 730 735  
 Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile  
 740 745 750  
 Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val  
 755 760 765  
 Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu  
 770 775 780  
 Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp Gly  
 785 790 795 800  
 Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile Met  
 805 810 815  
 Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu  
 820 825 830  
 Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val  
 835 840 845  
 Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val  
 850 855 860  
 Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro  
 865 870 875 880  
 Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro Met

885                      890                      895  
 Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu  
 900                      905                      910  
 Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp Glu  
 915                      920                      925  
 Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe  
 930                      935                      940  
 Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro  
 945                      950                      955                      960  
 Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro Val  
 965                      970                      975  
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 Pro Ala Ile Leu Glu  
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<220>

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 ggctcctgac ca atg ggg aag tgg cat gtg gga ggg cgc cgg ggt tcc ccc 171

Met Gly Lys Trp His Val Gly Gly Arg Arg Gly Ser Pro

1 5 10

cgc caa tgg gga gct acg gcg cgc ggc cgg gac ttg gag gcg gtg cgg 219

Arg Gln Trp Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg

15 20 25

cgc ggc ggg tgc ggt tca gtc ggt cgg cgg cgg cag cgg agg agg agg 267

Arg Gly Gly Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg

30 35 40 45

agg agg agg agg atg agg agg atg agg agg atg tgg gcc acg cag ggg 315

Arg Arg Arg Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly

50 55 60

ctg gcg gtg cgc gtg gct ctg agc gtg ctg ccg ggc agc cgg gcg ctg 363

Leu Ala Val Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu

65 70 75

cgg ccg ggc gac tgc gaa gtt tgt att tct tat ctg gga aga ttt tac 411

Arg Pro Gly Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr

80 85 90

cag gac ctc aaa gac aga gat gtc aca ttc tca cca gcc act att gaa 459

Gln Asp Leu Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu

95 100 105

aac gaa ctt ata aag ttc tgc cgg gaa gca aga ggc aaa gag aat cgg 507

Asn Glu Leu Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg

110 115 120 125

ttg tgc tac tat atc ggg gcc aca gat gat gca gcc acc aaa atc atc 555

Leu Cys Tyr Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile

130 135 140

aat gag gla tca aag cct ctg gcc cac cac atc cct glg gag aag atc 603  
 Asn Glu Val Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile  
 145 150 155  
 tgt gag aag ctt aag aag aag gac agc cag ata tgt gag ctt aag tat 651  
 Cys Glu Lys Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr  
 160 165 170  
 gac aag cag atc gac ctg agc aca glg gac ctg aag aag ctc cga gtt 699  
 Asp Lys Gln Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val  
 175 180 185  
 aaa gag ctg aag aag att ctg gat gac tgg ggg gag aca tgc aaa ggc 747  
 Lys Glu Leu Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly  
 190 195 200 205  
 tgt gca gaa aag tct gac tac atc cgg aag ata aat gaa ctg atg cct 795  
 Cys Ala Glu Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro  
 210 215 220  
 aaa tat gcc ccc aag gca gcc agt gca ccg acc gat ttg tagtctgctc 844  
 Lys Tyr Ala Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu  
 225 230  
 aatctctgtt gcaccigagg gggaaaaaac agttcaactg cttaciccga aaacagcctt 904  
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&lt;210&gt; 30

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

Met Gly Lys Trp His Val Gly Gly Arg Arg Gly Ser Pro Arg Gln Trp

1

5

10

15

Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg Arg Gly Gly

20

25

30

Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg Arg Arg Arg

35

40

45

Arg Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly Leu Ala Val

50

55

60

Arg Val Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu Arg Pro Gly

65

70

75

80

Asp Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr Gln Asp Leu

85

90

95

Lys Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu Asn Glu Leu

100

105

110

Ile Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg Leu Cys Tyr

115

120

125

Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile Asn Glu Val

130

135

140

Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile Cys Glu Lys

145

150

155

160

Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr Asp Lys Gln

165

170

175

Ile Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val Lys Glu Leu

180

185

190

Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly Cys Ala Glu

195                      200                      205  
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 210                      215                      220  
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    Met Glu Ser Glu Thr Glu Pro  
    1                      5  
  
 gag ccc gtc acg ctc ctg glg aag agc ccc aac cag cgc cac cgc gac 162  
 Glu Pro Val Thr Leu Leu Val Lys Ser Pro Asn Gln Arg His Arg Asp  
    10                      15                      20  
  
 ttg gag ctg agt ggc gac cgc ggc tgg agt gtg ggc cac ctc aag gcc 210  
 Leu Glu Leu Ser Gly Asp Arg Gly Trp Ser Val Gly His Leu Lys Ala  
    25                      30                      35  
  
 cac ctg agc cgc gtc tac ccc gag cgt ccg cgt cca gag gac cag agg 258  
 His Leu Ser Arg Val Tyr Pro Glu Arg Pro Arg Pro Glu Asp Gln Arg  
    40                      45                      50                      55



tta att tat tct ggg aag ctg ttg ttg gat cac caa tgt ctc agg gac 306  
 Leu Ile Tyr Ser Gly Lys Leu Leu Leu Asp His Gln Cys Leu Arg Asp  
 60 65 70  
 ttg ctt cca aag cag gaa aaa cgg cat gtt ttg cat ctg gtg tgc aat 354  
 Leu Leu Pro Lys Gln Glu Lys Arg His Val Leu His Leu Val Cys Asn  
 75 80 85  
 gtg aag agt cct tca aaa atg cca gaa atc aac gcc aag gtg gct gaa 402  
 Val Lys Ser Pro Ser Lys Met Pro Glu Ile Asn Ala Lys Val Ala Glu  
 90 95 100  
 tcc aca gag gag cct gct ggt tct aat cgg gga cag tat cct gag gat 450  
 Ser Thr Glu Glu Pro Ala Gly Ser Asn Arg Gly Gln Tyr Pro Glu Asp  
 105 110 115  
 tcc tca agt gat ggt tta agg caa agg gaa gtt ctt cgg aac ctt tct 498  
 Ser Ser Ser Asp Gly Leu Arg Gln Arg Glu Val Leu Arg Asn Leu Ser  
 120 125 130 135  
 tcc cct gga tgg gaa aac atc tca agg cct gaa gct gcc cag cag gca 546  
 Ser Pro Gly Trp Glu Asn Ile Ser Arg Pro Glu Ala Ala Gln Gln Ala  
 140 145 150  
 ttc caa ggc ctg ggt cct ggt ttc tcc ggt tac aca ccc tat ggg tgg 594  
 Phe Gln Gly Leu Gly Pro Gly Phe Ser Gly Tyr Thr Pro Tyr Gly Trp  
 155 160 165  
 ctt cag ctt tcc tgg ttc cag cag ata tat gca cga cag tac tac atg 642  
 Leu Gln Leu Ser Trp Phe Gln Gln Ile Tyr Ala Arg Gln Tyr Tyr Met  
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 caa tat tta gca gcc act gct gca tca ggg gct ttt gtt cca cca cca 690  
 Gln Tyr Leu Ala Ala Thr Ala Ala Ser Gly Ala Phe Val Pro Pro Pro

185	190	195	
agt gca caa gag ata cct gtg gtc tct gca cct gct cca gcc cct att			738
Ser Ala Gln Glu Ile Pro Val Val Ser Ala Pro Ala Pro Ala Pro Ile			
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cac aac cag ttt cca gct gaa aac cag cct gcc aat cag aat gct gct			786
His Asn Gln Phe Pro Ala Glu Asn Gln Pro Ala Asn Gln Asn Ala Ala			
	220	225	230
cct caa gtg gtt gtt aat cct gga gcc aat caa aat ttg cgg atg aat			834
Pro Gln Val Val Val Asn Pro Gly Ala Asn Gln Asn Leu Arg Met Asn			
	235	240	245
gca caa ggt ggc cct att gtg gaa gaa gat gat gaa ata aat cga gat			882
Ala Gln Gly Gly Pro Ile Val Glu Glu Asp Asp Glu Ile Asn Arg Asp			
	250	255	260
tgg ttg gat tgg acc tat tca gca gct aca ttt tct gtt ttt ctc agt			930
Trp Leu Asp Trp Thr Tyr Ser Ala Ala Thr Phe Ser Val Phe Leu Ser			
	265	270	275
atc ctc tac ttc tac tcc tcc ctg agc aga ttc ctc atg gtc atg ggg			978
Ile Leu Tyr Phe Tyr Ser Ser Leu Ser Arg Phe Leu Met Val Met Gly			
280	285	290	295
gcc acc gtt gtt atg tac ctg cat cac gtt ggg tgg ttt cca ttt aga			1026
Ala Thr Val Val Met Tyr Leu His His Val Gly Trp Phe Pro Phe Arg			
	300	305	310
ccg agg ccg gtt cag aac ttc cca aat gat ggt cct cct cct gac gtt			1074
Pro Arg Pro Val Gln Asn Phe Pro Asn Asp Gly Pro Pro Pro Asp Val			
	315	320	325
gta aat cag gac ccc aac aat aac tta cag gaa ggc act gat cct gaa			1122
Val Asn Gln Asp Pro Asn Asn Asn Leu Gln Glu Gly Thr Asp Pro Glu			

330 335 340  
act gaa gac ccc aac cac ctc cct cca gac agg gat gta cta gat ggc 1170  
Thr Glu Asp Pro Asn His Leu Pro Pro Asp Arg Asp Val Leu Asp Gly  
345 350 355  
gag cag acc agc ccc tcc ttt atg agc aca gca tgg ctt gtc ttc aag 1218  
Glu Gln Thr Ser Pro Ser Phe Met Ser Thr Ala Trp Leu Val Phe Lys  
360 365 370 375  
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Thr Phe Phe Ala Ser Leu Leu Pro Glu Gly Pro Pro Ala Ile Ala Asn  
380 385 390  
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<210> 32

<211> 391

<212> PRT

<213> Homo sapiens

<400> 32

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20 25 30  
Ser Val Gly His Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg  
35 40 45  
Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu  
50 55 60  
Asp His Gln Cys Leu Arg Asp Leu Leu Pro Lys Gln Glu Lys Arg His  
65 70 75 80  
Val Leu His Leu Val Cys Asn Val Lys Ser Pro Ser Lys Met Pro Glu  
85 90 95  
Ile Asn Ala Lys Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn  
100 105 110  
Arg Gly Gln Tyr Pro Glu Asp Ser Ser Ser Asp Gly Leu Arg Gln Arg  
115 120 125  
Glu Val Leu Arg Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg  
130 135 140  
Pro Glu Ala Ala Gln Gln Ala Phe Gln Gly Leu Gly Pro Gly Phe Ser  
145 150 155 160  
Gly Tyr Thr Pro Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile  
165 170 175  
Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser  
180 185 190  
Gly Ala Phe Val Pro Pro Pro Ser Ala Gln Glu Ile Pro Val Val Ser  
195 200 205  
Ala Pro Ala Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln

210 215 220  
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225 230 235 240  
Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Ile Val Glu Glu  
245 250 255  
Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala  
260 265 270  
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Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His  
290 295 300  
Val Gly Trp Phe Pro Phe Arg Pro Arg Pro Val Gln Asn Phe Pro Asn  
305 310 315 320  
Asp Gly Pro Pro Pro Asp Val Val Asn Gln Asp Pro Asn Asn Asn Leu  
325 330 335  
Gln Glu Gly Thr Asp Pro Glu Thr Glu Asp Pro Asn His Leu Pro Pro  
340 345 350  
Asp Arg Asp Val Leu Asp Gly Glu Gln Thr Ser Pro Ser Phe Met Ser  
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Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu  
370 375 380  
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&lt;210&gt; 33

&lt;211&gt; 4067

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (812).. (1138)

&lt;400&gt; 33

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Met Ser Ala Arg Gly Glu Gly

1

5

gcg ggg cag ccg tcc act tca gcc cag gga caa cct gcc gcc cca gcg 880

Ala Gly Gln Pro Ser Thr Ser Ala Gln Gly Gln Pro Ala Ala Pro Ala

10

15

20

cct cag aag aga gga cgc ggc cgc ccc agg aag cag cag caa gaa cca 928

Pro Gln Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln Gln Gln Glu Pro

25

30

35

acc ggt gag ccc tct cct aag aga ccc agg gga aga ccc aaa ggc agc 976  
 Thr Gly Glu Pro Ser Pro Lys Arg Pro Arg Gly Arg Pro Lys Gly Ser  
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 Lys Asn Lys Ser Pro Ser Lys Ala Ala Gln Lys Lys Ala Glu Ala Thr  
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 gga gaa aaa cgg cca aga ggc aga cct agg aaa tgg cca caa caa gtt 1072  
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<210> 34

<211> 109

<212> PRT

<213> Homo sapiens

<400> 34

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Gly Gln Pro Ala Ala Pro Ala Pro Gln Lys Arg Gly Arg Gly Arg Pro

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Arg Lys Gln Gln Gln Glu Pro Thr Gly Glu Pro Ser Pro Lys Arg Pro

35 40 45

Arg Gly Arg Pro Lys Gly Ser Lys Asn Lys Ser Pro Ser Lys Ala Ala

50 55 60

Gln Lys Lys Ala Glu Ala Thr Gly Glu Lys Arg Pro Arg Gly Arg Pro

65 70 75 80

Arg Lys Trp Pro Gln Gln Val Val Gln Lys Lys Pro Ala Gln Glu Glu

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90

95

Thr Glu Glu Thr Ser Ser Gln Glu Ser Ala Glu Glu Asp

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105

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<212> DNA

<213> Homo sapiens

<220>

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<222> (148).. (1032)

<400> 35

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cccagctgcc caggaagagc cccagcc atg gaa cac cag ctc ctg tgc tgc gaa 174

Met Glu His Gln Leu Leu Cys Cys Glu

1

5

gtg gaa acc atc cgc cgc gcg tac ccc gat gcc aac ctc ctc aac gac 222

Val Glu Thr Ile Arg Arg Ala Tyr Pro Asp Ala Asn Leu Leu Asn Asp

10

15

20

25

cgg gtg ctg cgg gcc atg ctg aag gcg gag gag acc tgc gcg ccc tcg 270

Arg Val Leu Arg Ala Met Leu Lys Ala Glu Glu Thr Cys Ala Pro Ser

30

35

40

gtg tcc tac ttc aaa tgt gtg cag aag gag gtc ctg ccg tcc atg cgg 318

Val Ser Tyr Phe Lys Cys Val Gln Lys Glu Val Leu Pro Ser Met Arg

45

50

55

aag atc gtc gcc acc tgg atg ctg gag gtc tgc gag gaa cag aag tgc 366  
Lys Ile Val Ala Thr Trp Met Leu Glu Val Cys Glu Glu Gln Lys Cys  
60 65 70  
gag gag gag gtc ttc ccg ctg gcc atg aac tac ctg gac cgc ttc ctg 414  
Glu Glu Glu Val Phe Pro Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu  
75 80 85  
tcg ctg gag ccc gtg aaa aag agc cgc ctg cag ctg ctg ggg gcc act 462  
Ser Leu Glu Pro Val Lys Lys Ser Arg Leu Gln Leu Leu Gly Ala Thr  
90 95 100 105  
tgc atg ttc gtg gcc tct aag atg aag gag acc atc ccc ctg acg gcc 510  
Cys Met Phe Val Ala Ser Lys Met Lys Glu Thr Ile Pro Leu Thr Ala  
110 115 120  
gag aag ctg tgc atc tac acc gac aac tcc atc cgg ccc gag gag ctg 558  
Glu Lys Leu Cys Ile Tyr Thr Asp Asn Ser Ile Arg Pro Glu Glu Leu  
125 130 135  
ctg caa atg gag ctg ctc ctg gtg aac aag ctc aag tgg aac ctg gcc 606  
Leu Gln Met Glu Leu Leu Leu Val Asn Lys Leu Lys Trp Asn Leu Ala  
140 145 150  
gca atg acc ccg cac gat ttc att gaa cac ttc ctc tcc aaa atg cca 654  
Ala Met Thr Pro His Asp Phe Ile Glu His Phe Leu Ser Lys Met Pro  
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gag gcg gag gag aac aaa cag atc atc cgc aaa cac gcg cag acc ttc 702  
Glu Ala Glu Glu Asn Lys Gln Ile Ile Arg Lys His Ala Gln Thr Phe  
170 175 180 185  
gtt gcc ctc tgt gcc aca gat gtg aag ttc att tcc aat ccg ccc tcc 750  
Val Ala Leu Cys Ala Thr Asp Val Lys Phe Ile Ser Asn Pro Pro Ser

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Met Val Ala Ala Gly Ser Val Val Ala Ala Val Gln Gly Leu Asn Leu			
205	210	215	
agg agc ccc aac aac ttc ctg tcc tac tac cgc ctc aca cgc ttc ctc			846
Arg Ser Pro Asn Asn Phe Leu Ser Tyr Tyr Arg Leu Thr Arg Phe Leu			
220	225	230	
tcc aga gtg atc aag tgt gac cca gac tgc ctc cgg gcc tgc cag gag			894
Ser Arg Val Ile Lys Cys Asp Pro Asp Cys Leu Arg Ala Cys Gln Glu			
235	240	245	
cag atc gaa gcc ctg ctg gag tca agc ctg cgc cag gcc cag cag aac			942
Gln Ile Glu Ala Leu Leu Glu Ser Ser Leu Arg Gln Ala Gln Gln Asn			
250	255	260	265
atg gac ccc aag gcc gcc gag gag gag gaa gag gag gag gag gag gtg			990
Met Asp Pro Lys Ala Ala Glu Glu Glu Glu Glu Glu Glu Glu Val			
270	275	280	
gac ctg gct tgc aca ccc acc gac gtg cgg gac gtg gac atc			1032
Asp Leu Ala Cys Thr Pro Thr Asp Val Arg Asp Val Asp Ile			
285	290	295	
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<210> 36

<211> 295

<212> PRT

<213> Homo sapiens

<400> 36

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Lys Ala Glu Glu Thr Cys Ala Pro Ser Val Ser Tyr Phe Lys Cys Val			
35	40	45	
Gln Lys Glu Val Leu Pro Ser Met Arg Lys Ile Val Ala Thr Trp Met			
50	55	60	
Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu			
65	70	75	80
Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Leu Glu Pro Val Lys Lys			
85	90	95	
Ser Arg Leu Gln Leu Leu Gly Ala Thr Cys Met Phe Val Ala Ser Lys			
100	105	110	
Met Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr			
115	120	125	
Asp Asn Ser Ile Arg Pro Glu Glu Leu Leu Gln Met Glu Leu Leu Leu			
130	135	140	
Val Asn Lys Leu Lys Trp Asn Leu Ala Ala Met Thr Pro His Asp Phe			
145	150	155	160
Ile Glu His Phe Leu Ser Lys Met Pro Glu Ala Glu Glu Asn Lys Gln			
165	170	175	
Ile Ile Arg Lys His Ala Gln Thr Phe Val Ala Leu Cys Ala Thr Asp			
180	185	190	
Val Lys Phe Ile Ser Asn Pro Pro Ser Met Val Ala Ala Gly Ser Val			
195	200	205	
Val Ala Ala Val Gln Gly Leu Asn Leu Arg Ser Pro Asn Asn Phe Leu			
210	215	220	

Ser Tyr Tyr Arg Leu Thr Arg Phe Leu Ser Arg Val Ile Lys Cys Asp

225 230 235 240

Pro Asp Cys Leu Arg Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Glu

245 250 255

Ser Ser Leu Arg Gln Ala Gln Gln Asn Met Asp Pro Lys Ala Ala Glu

260 265 270

Glu Glu Glu Glu Glu Glu Glu Glu Val Asp Leu Ala Cys Thr Pro Thr

275 280 285

Asp Val Arg Asp Val Asp Ile

290 295

<210> 37

<211> 5007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (436).. (3402)

<400> 37

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 ttggatagct gccgcccggg agaggtagacc cgggcgccct gctagggtag aggccctgc 420  
 cctcgccccg ggatc atg aaa ggc ctc ggt gac agc cgc ccc cgc cac ctc 471



Met Lys Gly Leu Gly Asp Ser Arg Pro Arg His Leu

1 5 10

tcc gac agc cta gac cca ccc cac gag ccc ctg ttt gca ggg acc gac 519

Ser Asp Ser Leu Asp Pro Pro His Glu Pro Leu Phe Ala Gly Thr Asp

15 20 25

cgc aac ccc tac ctg ctg tgc ccc acg gag gcc ttc gcc cgc gag gcc 567

Arg Asn Pro Tyr Leu Leu Ser Pro Thr Glu Ala Phe Ala Arg Glu Ala

30 35 40

cgc ttc ccc ggg cag aac acc ctg cca gga gat ggc ctc ttt ccc ctc 615

Arg Phe Pro Gly Gln Asn Thr Leu Pro Gly Asp Gly Leu Phe Pro Leu

45 50 55 60

aac aac cag ctg ccc ccg ccc agc agc acc ttt ccc cgc atc cac tac 663

Asn Asn Gln Leu Pro Pro Pro Ser Ser Thr Phe Pro Arg Ile His Tyr

65 70 75

aac tcc cac ttc gag gtg cca gag gag agc ccc ttc ccc agc cat gcc 711

Asn Ser His Phe Glu Val Pro Glu Glu Ser Pro Phe Pro Ser His Ala

80 85 90

caa gcc acc aag atc aac cgg ctg ccc gcc aac ctc ctg gac cag ttt 759

Gln Ala Thr Lys Ile Asn Arg Leu Pro Ala Asn Leu Leu Asp Gln Phe

95 100 105

gag aag cag ctg ccc atc cac cgt gat ggc ttc agc acc ctc caa ttt 807

Glu Lys Gln Leu Pro Ile His Arg Asp Gly Phe Ser Thr Leu Gln Phe

110 115 120

ccc cgt ggc gag gcc aag gcc cgt ggt gag agc cct ggc cgc atc cgc 855

Pro Arg Gly Glu Ala Lys Ala Arg Gly Glu Ser Pro Gly Arg Ile Arg

125 130 135 140

cac ctg gtc cac tca gtc cag cgg ctt ttc ttc acc aag gca ccc tca 903  
 His Leu Val His Ser Val Gln Arg Leu Phe Phe Thr Lys Ala Pro Ser  
 145 150 155  
 ctg gag ggc aca gcg ggc aag gtc ggt ggc aat ggc agc aag aag ggt 951  
 Leu Glu Gly Thr Ala Gly Lys Val Gly Gly Asn Gly Ser Lys Lys Gly  
 160 165 170  
 ggc atg gag gac ggc aag ggc cgg agg gcc aaa agc aag gag cgg gcc 999  
 Gly Met Glu Asp Gly Lys Gly Arg Arg Ala Lys Ser Lys Glu Arg Ala  
 175 180 185  
 aag gct ggg gag ccc aaa cgg cgc agc cgc tcc aac atc tca ggc tgg 1047  
 Lys Ala Gly Glu Pro Lys Arg Arg Ser Arg Ser Asn Ile Ser Gly Trp  
 190 195 200  
 tgg agc tcc gat gac aac ttg gac ggc gag gcc ggc gcc ttc cgc agc 1095  
 Trp Ser Ser Asp Asp Asn Leu Asp Gly Glu Ala Gly Ala Phe Arg Ser  
 205 210 215 220  
 agt ggc cca gcc tct ggg ctg atg ata cta ggc cgc cag gca gaa cgc 1143  
 Ser Gly Pro Ala Ser Gly Leu Met Ile Leu Gly Arg Gln Ala Glu Arg  
 225 230 235  
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 Ser Gln Pro Arg Tyr Phe Met His Ala Tyr Asn Thr Ile Ser Gly His  
 240 245 250  
 atg ctc aaa acc acc aag aac aac act act gag ctg act gcc cca cca 1239  
 Met Leu Lys Thr Thr Lys Asn Asn Thr Thr Glu Leu Thr Ala Pro Pro  
 255 260 265  
 ccc ccg ccc gca ccc cca gcc acc tgc ccc agc ctt ggg gtg ggc act 1287  
 Pro Pro Pro Ala Pro Pro Ala Thr Cys Pro Ser Leu Gly Val Gly Thr  
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gac acc aac tac gtc aaa cgg ggc tcc tgg tcc act ctg acc ctc agc 1335  
 Asp Thr Asn Tyr Val Lys Arg Gly Ser Trp Ser Thr Leu Thr Leu Ser  
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 cac gcc cac gag gtc tgc cag aag acc tca gcc acc ttg gat aag agc 1383  
 His Ala His Glu Val Cys Gln Lys Thr Ser Ala Thr Leu Asp Lys Ser  
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 ctg ctc aag tcc aaa tcc tgc cac cag ggt cta gcc tac cat tac ctg 1431  
 Leu Leu Lys Ser Lys Ser Cys His Gln Gly Leu Ala Tyr His Tyr Leu  
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 Ser Gly Gly Ser Pro Lys Pro Ser Pro Lys Thr Ala Ala Arg Arg Gln  
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 Ser Tyr Leu Arg Ala Thr Gln Gln Ser Leu Gly Glu Gln Ser Asn Pro  
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 cgc agg agt ctg gac cgc ctg gat tca gtg gac atg ctg ctg ccc tcc 1719  
 Arg Arg Ser Leu Asp Arg Leu Asp Ser Val Asp Met Leu Leu Pro Ser

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Lys Cys Pro Ser Trp Glu Glu Asp Tyr Thr Pro Val Ser Asp Ser Leu			
430	435	440	
aac gac tcc agc tgc atc agc cag att ttt gga cag gcc tcc ctg atc			1815
Asn Asp Ser Ser Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile			
445	450	455	460
ccc cag ttg ttt ggc cat gag cag cag gta cgg gag gca gag ctg agt			1863
Pro Gln Leu Phe Gly His Glu Gln Gln Val Arg Glu Ala Glu Leu Ser			
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gac cag tat gag gcg gcc tgc gag tca gcc tgc agt gaa gcg gag tcc			1911
Asp Gln Tyr Glu Ala Ala Cys Glu Ser Ala Cys Ser Glu Ala Glu Ser			
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aca gcg gca gag acg ctt gac ttg cca ctg ccc agc tac ttc cgc tcc			1959
Thr Ala Ala Glu Thr Leu Asp Leu Pro Leu Pro Ser Tyr Phe Arg Ser			
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cgc agc cac agc tac ctg cgt gcc atc cag gca ggc tgc tcg cag gag			2007
Arg Ser His Ser Tyr Leu Arg Ala Ile Gln Ala Gly Cys Ser Gln Glu			
	510	515	520
gag gac agt gtc tcc ctg cag tcc ctc tcc cca ccg ccc agt acc ggc			2055
Glu Asp Ser Val Ser Leu Gln Ser Leu Ser Pro Pro Pro Ser Thr Gly			
525	530	535	540
agc ctc agc aat agt cgc acg ctt ccg agt tca tca tgc cta gtg gcg			2103
Ser Leu Ser Asn Ser Arg Thr Leu Pro Ser Ser Ser Cys Leu Val Ala			
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tat aag aag acc ccg cca ccg gtc cct cca cgc acc act tca aag ccg			2151
Tyr Lys Lys Thr Pro Pro Pro Val Pro Pro Arg Thr Thr Ser Lys Pro			

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ttc atc tca gtc aca gtc cag agc agt act gag tct gcc cag gac acc	2199		
Phe Ile Ser Val Thr Val Gln Ser Ser Thr Glu Ser Ala Gln Asp Thr			
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tac ctg gac agc cag gac cac aag agc gag gtg act agc cag tcg ggc	2247		
Tyr Leu Asp Ser Gln Asp His Lys Ser Glu Val Thr Ser Gln Ser Gly			
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ctg agc aac tcg tcg gac agc ctg gac agc agt acc cga ccg ccc agc	2295		
Leu Ser Asn Ser Ser Asp Ser Leu Asp Ser Ser Thr Arg Pro Pro Ser			
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gtg aca cgg ggt gga gtc gcc cca gcc cct gag gcc cca gag cca ccc	2343		
Val Thr Arg Gly Gly Val Ala Pro Ala Pro Glu Ala Pro Glu Pro Pro			
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cca aaa cat gca gct ctg aaa agt gaa caa ggg acg ctg acc agc tct	2391		
Pro Lys His Ala Ala Leu Lys Ser Glu Gln Gly Thr Leu Thr Ser Ser			
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gag tcc cac ccc gag gcc gcc ccc aaa agg aaa ctg tca tcg ata gga	2439		
Glu Ser His Pro Glu Ala Ala Pro Lys Arg Lys Leu Ser Ser Ile Gly			
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ata caa gag agg act aga agg aac ggt tcc cac ctc tcg gag gac aac	2487		
Ile Gln Glu Arg Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn			
670	675	680	
gga ccc aaa gcg atc gat gtg atg gca ccc tcc tca gaa agc agc gtc	2535		
Gly Pro Lys Ala Ile Asp Val Met Ala Pro Ser Ser Glu Ser Ser Val			
685	690	695	700
ccc tct cac agt atg tcc tcc cga cgg gac aca gac tcg gat acc cag	2583		

Pro Ser His Ser Met Ser Ser Arg Arg Asp Thr Asp Ser Asp Thr Gln  
                     705                    710                    715  
 gat gcc aat gac tca agc tgt aag tca tct gag agg agc ctc ccg gac 2631  
 Asp Ala Asn Asp Ser Ser Cys Lys Ser Ser Glu Arg Ser Leu Pro Asp  
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 tgt acc cct cac ccc aac tcc atc agc atc gat gcc ggt ccc cgg cag 2679  
 Cys Thr Pro His Pro Asn Ser Ile Ser Ile Asp Ala Gly Pro Arg Gln  
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 gcc ccc aag att gcc cag atc aag cgc aac ctc tcc tat gga gac aac 2727  
 Ala Pro Lys Ile Ala Gln Ile Lys Arg Asn Leu Ser Tyr Gly Asp Asn  
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 agc gac cct gcc cta gag gcg tcc tcg ctg ccc cca ccc gac ccc tgg 2775  
 Ser Asp Pro Ala Leu Glu Ala Ser Ser Leu Pro Pro Pro Asp Pro Trp  
 765                    770                    775                    780  
 ctc gag acc tcc tcc agc tcc cca gca gag ccg gca cag cca ggg gcc 2823  
 Leu Glu Thr Ser Ser Ser Ser Pro Ala Glu Pro Ala Gln Pro Gly Ala  
                     785                    790                    795  
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 Cys Arg Arg Asp Gly Tyr Trp Phe Leu Lys Leu Leu Gln Ala Glu Thr  
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 gag cgg ctg gaa ggc tgg tgc tgc cag atg gac aag gag acc aaa gag 2919  
 Glu Arg Leu Glu Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu  
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 aac aac ctc tct gaa gaa gtc tta gga aaa gtc ctc agt gct gtg ggc 2967  
 Asn Asn Leu Ser Glu Glu Val Leu Gly Lys Val Leu Ser Ala Val Gly  
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Ser Ala Gln Leu Leu Met Ser Gln Lys Phe Gln Gln Phe Arg Gly Leu  
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 Cys Glu Gln Asn Leu Asn Pro Asp Ala Asn Pro Arg Pro Thr Ala Gln  
 865 870 875  
 gac ctg gca ggg ttc tgg gac ctg cta cag ctg tcc atc gag gat atc 3111  
 Asp Leu Ala Gly Phe Trp Asp Leu Leu Gln Leu Ser Ile Glu Asp Ile  
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 Ser Met Lys Phe Asp Glu Leu Tyr His Leu Lys Ala Asn Ser Trp Gln  
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 Pro Val Pro Lys Lys Pro Ala Lys Ser Lys Pro Ala Val Ser Arg Asp  
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 945 950 955  
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 960 965 970  
 gag agc gca gac agc atc gag att tat gtc ccg gag gcc cag acc agg 3399  
 Glu Ser Ala Asp Ser Ile Glu Ile Tyr Val Pro Glu Ala Gln Thr Arg  
 975 980 985

ctc lgagaccatg caggaggaaa gaaacgatit taaatcatta aaaacacaaa 3452

Leu

aactaagtgc gaacggaaca gagttttctc aacctttgct atggttattc tgtctagaga 3512

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<211> 989

<212> PRT

<213> Homo sapiens

<400> 38

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Asp Pro Pro His Glu Pro Leu Phe Ala Gly Thr Asp Arg Asn Pro Tyr

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Leu Leu Ser Pro Thr Glu Ala Phe Ala Arg Glu Ala Arg Phe Pro Gly

35 40 45

Gln Asn Thr Leu Pro Gly Asp Gly Leu Phe Pro Leu Asn Asn Gln Leu

50 55 60

Pro Pro Pro Ser Ser Thr Phe Pro Arg Ile His Tyr Asn Ser His Phe

65 70 75 80

Glu Val Pro Glu Glu Ser Pro Phe Pro Ser His Ala Gln Ala Thr Lys

85 90 95

Ile Asn Arg Leu Pro Ala Asn Leu Leu Asp Gln Phe Glu Lys Gln Leu

100 105 110

Pro Ile His Arg Asp Gly Phe Ser Thr Leu Gln Phe Pro Arg Gly Glu

115 120 125

Ala Lys Ala Arg Gly Glu Ser Pro Gly Arg Ile Arg His Leu Val His

130 135 140

Ser Val Gln Arg Leu Phe Phe Thr Lys Ala Pro Ser Leu Glu Gly Thr

145 150 155 160

Ala Gly Lys Val Gly Gly Asn Gly Ser Lys Lys Gly Gly Met Glu Asp  
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 Gly Lys Gly Arg Arg Ala Lys Ser Lys Glu Arg Ala Lys Ala Gly Glu  
 180 185 190  
 Pro Lys Arg Arg Ser Arg Ser Asn Ile Ser Gly Trp Trp Ser Ser Asp  
 195 200 205  
 Asp Asn Leu Asp Gly Glu Ala Gly Ala Phe Arg Ser Ser Gly Pro Ala  
 210 215 220  
 Ser Gly Leu Met Ile Leu Gly Arg Gln Ala Glu Arg Ser Gln Pro Arg  
 225 230 235 240  
 Tyr Phe Met His Ala Tyr Asn Thr Ile Ser Gly His Met Leu Lys Thr  
 245 250 255  
 Thr Lys Asn Asn Thr Thr Glu Leu Thr Ala Pro Pro Pro Pro Pro Ala  
 260 265 270  
 Pro Pro Ala Thr Cys Pro Ser Leu Gly Val Gly Thr Asp Thr Asn Tyr  
 275 280 285  
 Val Lys Arg Gly Ser Trp Ser Thr Leu Thr Leu Ser His Ala His Glu  
 290 295 300  
 Val Cys Gln Lys Thr Ser Ala Thr Leu Asp Lys Ser Leu Leu Lys Ser  
 305 310 315 320  
 Lys Ser Cys His Gln Gly Leu Ala Tyr His Tyr Leu Gln Val Pro Gly  
 325 330 335  
 Gly Gly Gly Glu Trp Ser Thr Thr Leu Leu Ser Pro Arg Glu Thr Asp  
 340 345 350  
 Ala Ala Ala Glu Gly Pro Ile Pro Cys Arg Arg Met Arg Ser Gly Ser  
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Tyr Ile Lys Ala Met Gly Asp Glu Asp Ser Asp Glu Ser Gly Gly Ser  
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 Pro Lys Pro Ser Pro Lys Thr Ala Ala Arg Arg Gln Ser Tyr Leu Arg  
 385 390 395 400  
 Ala Thr Gln Gln Ser Leu Gly Glu Gln Ser Asn Pro Arg Arg Ser Leu  
 405 410 415  
 Asp Arg Leu Asp Ser Val Asp Met Leu Leu Pro Ser Lys Cys Pro Ser  
 420 425 430  
 Trp Glu Glu Asp Tyr Thr Pro Val Ser Asp Ser Leu Asn Asp Ser Ser  
 435 440 445  
 Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile Pro Gln Leu Phe  
 450 455 460  
 Gly His Glu Gln Gln Val Arg Glu Ala Glu Leu Ser Asp Gln Tyr Glu  
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 485 490 495  
 Thr Leu Asp Leu Pro Leu Pro Ser Tyr Phe Arg Ser Arg Ser His Ser  
 500 505 510  
 Tyr Leu Arg Ala Ile Gln Ala Gly Cys Ser Gln Glu Glu Asp Ser Val  
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 Ser Leu Gln Ser Leu Ser Pro Pro Pro Ser Thr Gly Ser Leu Ser Asn  
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 Ser Arg Thr Leu Pro Ser Ser Ser Cys Leu Val Ala Tyr Lys Lys Thr  
 545 550 555 560  
 Pro Pro Pro Val Pro Pro Arg Thr Thr Ser Lys Pro Phe Ile Ser Val  
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 Thr Val Gln Ser Ser Thr Glu Ser Ala Gln Asp Thr Tyr Leu Asp Ser

580 585 590  
Gln Asp His Lys Ser Glu Val Thr Ser Gln Ser Gly Leu Ser Asn Ser  
595 600 605  
Ser Asp Ser Leu Asp Ser Ser Thr Arg Pro Pro Ser Val Thr Arg Gly  
610 615 620  
Gly Val Ala Pro Ala Pro Glu Ala Pro Glu Pro Pro Pro Lys His Ala  
625 630 635 640  
Ala Leu Lys Ser Glu Gln Gly Thr Leu Thr Ser Ser Glu Ser His Pro  
645 650 655  
Glu Ala Ala Pro Lys Arg Lys Leu Ser Ser Ile Gly Ile Gln Glu Arg  
660 665 670  
Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn Gly Pro Lys Ala  
675 680 685  
Ile Asp Val Met Ala Pro Ser Ser Glu Ser Ser Val Pro Ser His Ser  
690 695 700  
Met Ser Ser Arg Arg Asp Thr Asp Ser Asp Thr Gln Asp Ala Asn Asp  
705 710 715 720  
Ser Ser Cys Lys Ser Ser Glu Arg Ser Leu Pro Asp Cys Thr Pro His  
725 730 735  
Pro Asn Ser Ile Ser Ile Asp Ala Gly Pro Arg Gln Ala Pro Lys Ile  
740 745 750  
Ala Gln Ile Lys Arg Asn Leu Ser Tyr Gly Asp Asn Ser Asp Pro Ala  
755 760 765  
Leu Glu Ala Ser Ser Leu Pro Pro Pro Asp Pro Trp Leu Glu Thr Ser  
770 775 780  
Ser Ser Ser Pro Ala Glu Pro Ala Gln Pro Gly Ala Cys Arg Arg Asp

785                      790                      795                      800  
Gly Tyr Trp Phe Leu Lys Leu Leu Gln Ala Glu Thr Glu Arg Leu Glu  
                         805                      810                      815  
Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu Asn Asn Leu Ser  
                         820                      825                      830  
Glu Glu Val Leu Gly Lys Val Leu Ser Ala Val Gly Ser Ala Gln Leu  
                         835                      840                      845  
Leu Met Ser Gln Lys Phe Gln Gln Phe Arg Gly Leu Cys Glu Gln Asn  
                         850                      855                      860  
Leu Asn Pro Asp Ala Asn Pro Arg Pro Thr Ala Gln Asp Leu Ala Gly  
865                      870                      875                      880  
Phe Trp Asp Leu Leu Gln Leu Ser Ile Glu Asp Ile Ser Met Lys Phe  
                         885                      890                      895  
Asp Glu Leu Tyr His Leu Lys Ala Asn Ser Trp Gln Leu Val Glu Thr  
                         900                      905                      910  
Pro Glu Lys Arg Lys Glu Glu Lys Lys Pro Pro Pro Pro Val Pro Lys  
                         915                      920                      925  
Lys Pro Ala Lys Ser Lys Pro Ala Val Ser Arg Asp Lys Ala Ser Asp  
                         930                      935                      940  
Ala Ser Asp Lys Gln Arg Gln Glu Ala Arg Lys Arg Leu Leu Ala Ala  
945                      950                      955                      960  
Lys Arg Ala Ala Ser Val Arg Gln Asn Ser Ala Thr Glu Ser Ala Asp  
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&lt;210&gt; 39

&lt;211&gt; 2522

&lt;212&gt; DNA

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (1545)

&lt;400&gt; 39

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10

15

cgg ggc cag gtg gcc aag ctt gag gca gcc cta ggt gag gcc aag aag 96

Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu Gly Glu Ala Lys Lys

20

25

30

caa ctt cag gat gag atg ctg cgg cgg gtg gat gct gag aac agg ctg 144

Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu

35

40

45

cag acc atg aag gag gaa ctg gac ttc cag aag aac atc tac agt gag 192

Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu

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55

60

gag ctg cgt gag acc aag cgc cgt cat gag acc cga ctg gtg gag att 240

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70

75

80

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85

90

95

cag gaa ctg cgg gcc cag cat gag gac cag gtg gag cag tat aag aag 336

Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys

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Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser			
115	120	125	
gct gag agg aac agc aac ctg gtg ggg gct gcc cac gag gag ctg cag			432
Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln			
130	135	140	
cag tgc cgc atc cgc atc gac agc ctc tct gcc cag ctc agc cag ctc			480
Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu			
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cag aag cag ctg gca gcc aag gag gcg aag ctt cga gac ctg gag gac			528
Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu Arg Asp Leu Glu Asp			
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Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg Leu Leu Ala Glu Lys			
180	185	190	
gag cgg gag atg gcc gag atg cgg gca agg atg cag cag cag ctg gac			624
Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met Gln Gln Gln Leu Asp			
195	200	205	
gag tac cag gag ctt ctg gac atc aag ctg gcc ctg gac atg gag atc			672
Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala Leu Asp Met Glu Ile			
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cac gcc tac cgc aag ctc ttg gag ggc gag gag gag agg cta cgc ctg			720
His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Arg Leu			
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Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly Arg Ala Ser Ser His  
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 tca tcc cag aca cag ggt ggg ggc agc gtc acc aaa aag cgc aaa ctg 816  
 Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr Lys Lys Arg Lys Leu  
 260 265 270  
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 Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln His Ala Arg Thr Ser  
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 Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg  
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 Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met Gly Asn Trp Gln Ile  
 305 310 315 320  
 aag cgc cag aat gga gat gat ccc ttg ctg act tac cgg ttc cca cca 1008  
 Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr Tyr Arg Phe Pro Pro  
 325 330 335  
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Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val Arg Ser Val Thr Val  
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 Gly Ser Ser Ala Ser Ser Val Thr Val Thr Arg Ser Tyr Arg Ser Val  
 465 470 475 480  
 ggg ggc agt ggg ggt ggc agc ttc ggg gac aat ctg gtc acc cgc tcc 1488  
 Gly Gly Ser Gly Gly Gly Ser Phe Gly Asp Asn Leu Val Thr Arg Ser  
 485 490 495  
 tac ctc ctg ggc aac tcc agc ccc cga acc cag agc ccc cag aac tgc 1536  
 Tyr Leu Leu Gly Asn Ser Ser Pro Arg Thr Gln Ser Pro Gln Asn Cys  
 500 505 510  
 agc atc atg taatctggga cctgccaggc aggggtgggg gtggaggctt 1585  
 Ser Ile Met  
 515

cctgcgacct cctcaccica tgcccacccc ctgccctgca cgtcatggga gggggctlga 1645  
 agccaaagaa aaataaccct ttggttttt tcttctgtat tttttttct aagagaagtt 1705  
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 tatagaggct agcttctgct tttctgccct ggctgctgcc ccacccggg gacctgiga 1945  
 catggctcct gagaggcagg catagaggct tctccgccag cctcctctgg acggcaggct 2005  
 cactgccagg ccagctccg agagggagag agagagagag aggacagctt gagccgggcc 2065  
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<211> 515

<212> PRT

<213> Homo sapiens

<400> 40

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30

Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu

35 40 45  
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 Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg Leu Ala Asp Ala Leu  
 85 90 95  
 Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val Glu Gln Tyr Lys Lys  
 100 105 110  
 Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp Asn Ala Arg Gln Ser  
 115 120 125  
 Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln  
 130 135 140  
 Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala Gln Leu Ser Gln Leu  
 145 150 155 160  
 Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu Arg Asp Leu Glu Asp  
 165 170 175  
 Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg Leu Leu Ala Glu Lys  
 180 185 190  
 Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met Gln Gln Gln Leu Asp  
 195 200 205  
 Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala Leu Asp Met Glu Ile  
 210 215 220  
 His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Arg Leu  
 225 230 235 240  
 Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly Arg Ala Ser Ser His  
 245 250 255

Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr Lys Lys Arg Lys Leu  
 260 265 270  
 Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln His Ala Arg Thr Ser  
 275 280 285  
 Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg  
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 Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met Gly Asn Trp Gln Ile  
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 Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr Tyr Arg Phe Pro Pro  
 325 330 335  
 Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr Ile Trp Ala Ala Gly  
 340 345 350  
 Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu Val Trp Lys Ala Gln  
 355 360 365  
 Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr Ala Leu Ile Asn Ser  
 370 375 380  
 Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val Arg Ser Val Thr Val  
 385 390 395 400  
 Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp Leu Leu His His His  
 405 410 415  
 His Gly Ser His Cys Ser Ser Ser Gly Asp Pro Ala Glu Tyr Asn Leu  
 420 425 430  
 Arg Ser Arg Thr Val Leu Cys Gly Thr Cys Gly Gln Pro Ala Asp Lys  
 435 440 445  
 Ala Ser Ala Ser Gly Ser Gly Ala Gln Val Gly Gly Pro Ile Ser Ser  
 450 455 460

Gly Ser Ser Ala Ser Ser Val Thr Val Thr Arg Ser Tyr Arg Ser Val

465 470 475 480

Gly Gly Ser Gly Gly Gly Ser Phe Gly Asp Asn Leu Val Thr Arg Ser

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Tyr Leu Leu Gly Asn Ser Ser Pro Arg Thr Gln Ser Pro Gln Asn Cys

500 505 510

Ser Ile Met

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<211> 3474

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78).. (2813)

<400> 41

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cgagcgagag gcgcgga atg gtg gac tac cac gcg gcg aac cag tcg tac 110

Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr

1 5 10

cag tac ggc ccc agc agc gcg gca atg gct tgg cgg cgg ggg agc atg 158

Gln Tyr Gly Pro Ser Ser Ala Ala Met Ala Trp Arg Arg Gly Ser Met

15 20 25

ggc gac tac atg gcc cag gag gac gac tgg gac cgg gac ctg ctg ctg 206

Gly Asp Tyr Met Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu

30 35 40

gac ccg gcc tgg gag aag cag cag cgc aag acc ttc acg gca tgg agc 254  
 Asp Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser  
 45 50 55  
 aac tcc cac ctg cgg aag gca ggc aca cag atc gag aac att gat gag 302  
 Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu  
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 gac ttc cga gac ggg ctc aag ctc atg ctg ctc ctg gag gtc ata tca 350  
 Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser  
 80 85 90  
 ggg gag cgg tta cct aag ccg gag cgg ggg aag atg aga gtg cac aaa 398  
 Gly Glu Arg Leu Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys  
 95 100 105  
 atc aac aat gtg aac aaa gcg ctg gac ttt att gcc agc aaa ggg atc 446  
 Ile Asn Asn Val Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile  
 110 115 120  
 aag ctg gac ttc cat cgg gca gaa gag att gtg gac ggc aac gca aag 494  
 Lys Leu Asp Phe His Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys  
 125 130 135  
 atg acc ctg gga atg atc tgg acc atc atc ctt agg ttc gcc atc cag 542  
 Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln  
 140 145 150 155  
 gac atc tcc gtg gaa gag acc tcg gcc aag gaa ggg ctc ctt ctc tgg 590  
 Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp  
 160 165 170  
 tgc cag aga aag aca gcc cca tat aag aac gtc aat gtg cag aac ttc 638  
 Cys Gln Arg Lys Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe  
 175 180 185

cac atc agc tgg aag gat ggt ctt gcc ttc aat gcc ctg atc cac cgg 686  
 His Ile Ser Trp Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg  
 190 195 200  
 cac aga cca gag ctg att gag tat gac aag ctg agg aag gac gac cct 734  
 His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro  
 205 210 215  
 gtc acc aac ctg aac aat gcc ttc gaa gtg gct gag aaa tac ctc gac 782  
 Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp  
 220 225 230 235  
 atc ccc aag atg ctg gat gca gag gac atc glg aac acg gcc cgg ccc 830  
 Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro  
 240 245 250  
 gac gag aag gcc ata atg acc tat gtg tcc agc ttc tac cat gcc ttt 878  
 Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe  
 255 260 265  
 tca gga gcg cag aag gct gaa act gaa act gcc gcc aac cgg atc tgt 926  
 Ser Gly Ala Gln Lys Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys  
 270 275 280  
 aag gtg ctg gct gtc aac caa gag aac tgc agc acc tcg atg gag gac 974  
 Lys Val Leu Ala Val Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp  
 285 290 295  
 tac gag aag ctg gcc agc gac ctc ctg gag tgg atc cgg cgc acc atc 1022  
 Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile  
 300 305 310 315  
 ccc tgg ctg gag gac cgt gtg ccc caa aag act atc cag gag atg cag 1070  
 Pro Trp Leu Glu Asp Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln

320	325	330	
cag aag ctg gag gac ttc cgc gac tac cgg cgt gtg cac aag ccg ccc	1118		
Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro			
335	340	345	
aag gtg cag gag aag tgc cag ctg gag atc aac ttc aac agc gtg cag	1166		
Lys Val Gln Glu Lys Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln			
350	355	360	
acc aag ctg cgc ctc agc aac cgg ccc gcc ttc atg ccc tcc gag ggc	1214		
Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly			
365	370	375	
aag atg gtc tcg gac atc aac aat ggc tgg cag cac ttg gag cag gct	1262		
Lys Met Val Ser Asp Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala			
380	385	390	395
gag aag ggc tac gag gag tgg ctg ctg aat gag att cgc agg ctg gag	1310		
Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu			
400	405	410	
cgg ctc gac cac ctg gca gag aag ttc cgg cag aaa gcc tcc atc cac	1358		
Arg Leu Asp His Leu Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His			
415	420	425	
gag gcc tgg act gac ggg aag gaa gcc atg ctg aag cac cgg gac tac	1406		
Glu Ala Trp Thr Asp Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr			
430	435	440	
gag acg gcc aca cta tcg gac atc aaa gcc ctc att cgc aag cac gag	1454		
Glu Thr Ala Thr Leu Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu			
445	450	455	
gcc ttc gag agc gac ctg gct gcg cac cag gac cgc gtg gag cag atc	1502		
Ala Phe Glu Ser Asp Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile			



460	465	470	475	
gcc gcc tcc gcc cag gag ctc aac gag ctg gai tac tac gac tcc cac				1550
Ala Ala Ser Ala Gln Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His				
	480	485	490	
aat gtc aac acc cgg tgc cag aag atc tgt gac cag tgg gac gcc ctc				1598
Asn Val Asn Thr Arg Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu				
	495	500	505	
ggc tct ctg aca cat agt cgc agg gaa gcc ctg gag aaa aca gag aag				1646
Gly Ser Leu Thr His Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys				
	510	515	520	
cag ctg gag gcc atc atc gac cag ctg cac ctg gaa tac gcc aag ccc				1694
Gln Leu Glu Ala Ile Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro				
	525	530	535	
gcg gcc ccc ttc aac aac tgg atg gag agc gcc atg gag gac ctc cag				1742
Ala Ala Pro Phe Asn Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln				
540	545	550	555	
gac atg ttc atc gtc cat acc atc gag gag att gag ggc ctg atc tca				1790
Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser				
	560	565	570	
gcc cat gac cag ttc aag tcc acc ctg ccg gac gcc gat agg gag cgc				1838
Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg				
	575	580	585	
gag gcc atc ctg cat cca caa gga ggc cag agg atc gct gag agc aac				1886
Glu Ala Ile Leu His Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn				
	590	595	600	
cac atc aag ctg tcg ggc agc aac ccc tac acc acc gtc acc ccg caa				1934

His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln  
 605 610 615  
 atc atc aac tcc aag tgg gag aag gtg cag cag ctg gtg cca aaa cgg 1982  
 Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg  
 620 625 630 635  
 gac cat gcc ctc ctg gag gag cag agc aag cag cag cag tcc aac gag 2030  
 Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu  
 640 645 650  
 cac ctg cgc cgc cag ttc gcc agc cag gcc aat gtt gtg ggg ccc tgg 2078  
 His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp  
 655 660 665  
 atc cag acc aag atg gag gag atc gcg atc tcc att gag atg aac ggg 2126  
 Ile Gln Thr Lys Met Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly  
 670 675 680  
 acc ctg gag gac cag ctg agc cac ctg aag cag tat gaa cgc agc atc 2174  
 Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile  
 685 690 695  
 gtg gac tac aag ccc aac ctg gac ctg ctg gag cag cag cac cag ctc 2222  
 Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu  
 700 705 710 715  
 atc cag gag gcc ctc atc ttc gac aac aag cac acc aac tat acc atg 2270  
 Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met  
 720 725 730  
 gag cac atc cgc gtg ggc tgg gag cag ctg ctc acc acc att gcc cgc 2318  
 Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg  
 735 740 745  
 acc atc aac gag gtg gag aac cag atc ctt acc cgc gac gcc aag ggc 2366

Thr Ile Asn Glu Val Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly  
 750 755 760  
 atc agc cag gag cag atg cag gag ttc cgg gcg tcc ttc aac cac ttc 2414  
 Ile Ser Gln Glu Gln Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe  
 765 770 775  
 gac aag gat cat ggc ggg gcg ctg ggg cga gga gtt caa ggc ctg cct 2462  
 Asp Lys Asp His Gly Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro  
 780 785 790 795  
 cat cag cct ggg cta cga cgt gga gaa cga ccg gca ggt gag gcc gag 2510  
 His Gln Pro Gly Leu Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu  
 800 805 810  
 ttc aac cgc atc atg agc ctg gtc gac ccc aac cat agc ggc ctt gtt 2558  
 Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val  
 815 820 825  
 acc ttc caa gcc ttc atc gac ttc atg tgc cgg gag acc acc gac acc 2606  
 Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr  
 830 835 840  
 gac acg gct gac cag gta atc act tcc ttc aag gtc cta gca ggg gac 2654  
 Asp Thr Ala Asp Gln Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp  
 845 850 855  
 aag aac ttc atc aca gct gag gag ctg cgg aga gag ctg ccc ccc gac 2702  
 Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp  
 860 865 870 875  
 cag gcc gag tac tgc atc gcc cgc atg gcg cca tac cag ggc cct gac 2750  
 Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp  
 880 885 890

ggc gtg cgc ggt gcc ctc gac tac aag tcc ttc tcc acg gcc tlg tat 2798

Gly Val Arg Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr

895

900

905

ggc gag agc gac ctg tgaggcccca gagacctgac ccaacacccc cgacgccctcc 2853

Gly Glu Ser Asp Leu

910

aggagcctgg cagccccaca gtcccatgcc tccactctgt atctatgcaa agcactctct 2913

ctgcagtctc cggggigggt ggggtggcag ggaggggctg gggcaggctc tctctctct 2973

ctctttgttg gttagccagg aggttcccc gaccaggttg gggagacttg gggccagcgc 3033

ttctgtgtcg gtaaatatgt atgatgtgt gtgtttttt aaccaaggag gggccagtgg 3093

attccacag cacaaccggt ccttccatg ccttgggatg cctcaccaca cccaggctct 3153

ttcctttgct ctgaggctcc ttcaaggcct ccccaatcca ggccaaagcc ccatgtgcct 3213

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tgggaccac ccagccctc tccccctct gtccagact cacttgccat tgccaggaga 3333

tggccccaac aagcaccctg cttttgcagc agaggagctg agttggcaga ccgggcccc 3393

ctgaaccgca ccccatcca ccagccctg ccttgcttg tctggcctca cgtgtctcag 3453

attttctaag aacaaaaaa a 3474

<210> 42

<211> 912

<212> PRT

<213> Homo sapiens

<400> 42

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Ser Ala Ala Met Ala Trp Arg Arg Gly Ser Met Gly Asp Tyr Met Ala

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Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu  
 35 40 45  
 Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Ser Asn Ser His Leu Arg  
 50 55 60  
 Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp Gly  
 65 70 75 80  
 Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Pro  
 85 90 95  
 Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val Asn  
 100 105 110  
 Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile Lys Leu Asp Phe His  
 115 120 125  
 Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly Met  
 130 135 140  
 Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu  
 145 150 155 160  
 Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr  
 165 170 175  
 Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp Lys  
 180 185 190  
 Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu Leu  
 195 200 205  
 Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu Asn  
 210 215 220  
 Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu  
 225 230 235 240  
 Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala Ile

245 250 255  
Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys  
260 265 270  
Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val  
275 280 285  
Asn Gln Glu Asn Cys Ser Thr Ser Met Glu Asp Tyr Glu Lys Leu Ala  
290 295 300  
Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp  
305 310 315 320  
Arg Val Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp  
325 330 335  
Phe Arg Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys  
340 345 350  
Cys Gln Leu Glu Ile Asn Phe Asn Ser Val Gln Thr Lys Leu Arg Leu  
355 360 365  
Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp  
370 375 380  
Ile Asn Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu  
385 390 395 400  
Glu Trp Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu  
405 410 415  
Ala Glu Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp  
420 425 430  
Gly Lys Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu  
435 440 445  
Ser Asp Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp

WO 01/25427

PCT/JP00/06840

450  
Leu Ala Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ser Ala Gln  
455  
460  
465  
Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg  
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480  
485  
Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His  
490  
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Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile  
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510  
515  
Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro Ala Ala Pro Phe Asn  
520  
525  
530  
Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val  
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545  
His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe  
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555  
560  
Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu His  
565  
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575  
580  
Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser  
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Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys  
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Trp Glu Lys Val Gln Gln Leu Val Thr Pro Lys Arg Asp His Ala Leu Leu  
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620  
625  
Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu His Leu Arg Arg Gln  
630  
635  
640  
Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met  
645  
650  
655  
660  
163/527

WO 01/25427

Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln  
 675 680 685  
 Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro  
 690 695 700  
 Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu  
 705 710 715 720  
 Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val  
 725 730 735  
 Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val  
 740 745 750  
 Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln  
 755 760 765  
 Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly  
 770 775 780  
 Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro His Gln Pro Gly Leu  
 785 790 795 800  
 Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu Phe Asn Arg Ile Met  
 805 810 815  
 Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe  
 820 825 830  
 Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln  
 835 840 845  
 Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr  
 850 855 860  
 Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys  
 865 870 875 880



Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Gly Val Arg Gly Ala

885

890

895

Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu

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905

910

<210> 43

<211> 8971

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (110).. (8224)

<400> 43

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Met Pro Ser

1

acg gag aag gac ctg gcg gag gac gcg ccg tgg aag aag atc cag cag 166

Thr Glu Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln

5

10

15

aac aca ttc acg cgc tgg tgc aat gag cac ctc aag tgc gtg ggc aag 214

Asn Thr Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Gly Lys

20

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30

35

cgc ctg acc gac ctg cag cgc gac ctc agc gac ggg ctc cgg ctc atc 262

Arg Leu Thr Asp Leu Gln Arg Asp Leu Ser Asp Gly Leu Arg Leu Ile

40

45

50

gcg ctg ctc gag gtg ctc agc cag aag cgc atg tac cgc aag ttc cat 310

Ala Leu Leu Glu Val Leu Ser Gln Lys Arg Met Tyr Arg Lys Phe His  
                     55                    60                    65  
 ccg cgc ccc aac ttc cgc caa atg aag ctg gag aac gtg tcc gtg gcc 358  
 Pro Arg Pro Asn Phe Arg Gln Met Lys Leu Glu Asn Val Ser Val Ala  
                     70                    75                    80  
 ctc gag ttc ctc gag cgc gag cac atc aag ctc gtg tcc ata gac agc 406  
 Leu Glu Phe Leu Glu Arg Glu His Ile Lys Leu Val Ser Ile Asp Ser  
                     85                    90                    95  
 aag gcc atc gtg gat ggg aac ctg aag ctg atc ctg ggc ctg atc tgg 454  
 Lys Ala Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly Leu Ile Trp  
 100                    105                    110                    115  
 acg ctg atc ctg cac tac tcc atc tcc atg ccc atg tgg gag gat gaa 502  
 Thr Leu Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Glu Asp Glu  
                     120                    125                    130  
 gat gat gag gat gcc cgc aaa cag acg ccc aag cag cgg ctg ctt ggc 550  
 Asp Asp Glu Asp Ala Arg Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly  
                     135                    140                    145  
 tgg atc cag aac aag gtg ccc cag ctg ccc atc acc aac ttc aac cgt 598  
 Trp Ile Gln Asn Lys Val Pro Gln Leu Pro Ile Thr Asn Phe Asn Arg  
                     150                    155                    160  
 gac tgg cag gac ggc aaa gct ctg ggc gcc ctg gtg gac aac tgc gcc 646  
 Asp Trp Gln Asp Gly Lys Ala Leu Gly Ala Leu Val Asp Asn Cys Ala  
                     165                    170                    175  
 ccc ggt ctc tgc ccc gac tgg gag gcc tgg gat ccc aac cag ccc gtg 694  
 Pro Gly Leu Cys Pro Asp Trp Glu Ala Trp Asp Pro Asn Gln Pro Val  
 180                    185                    190                    195  
 gag aac tcc cgg gag gcc atg cag cag gcc gac gac tgg ctt ggg gtg 742

Glu Asn Ser Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Val  
 200 205 210  
 ccc cag gtc att gcc cct gag gag att gtg gac ccc aac gtg gat gag 790  
 Pro Gln Val Ile Ala Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu  
 215 220 225  
 cat tct gtt atg acc tac ctg tcc cag ttc ccc aag gcc aag ctc aaa 838  
 His Ser Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys  
 230 235 240  
 cct ggt gcc cct gtt cga tcc aag cag ctg aac ccc aag aaa gcc atc 886  
 Pro Gly Ala Pro Val Arg Ser Lys Gln Leu Asn Pro Lys Lys Ala Ile  
 245 250 255  
 gcc tat ggg cct ggc atc gag cca cag ggc aac acc gtg ctg cag cct 934  
 Ala Tyr Gly Pro Gly Ile Glu Pro Gln Gly Asn Thr Val Leu Gln Pro  
 260 265 270 275  
 gcc cac ttc acc gtg cag acg gtg gac gcg ggc gtg ggc gag gtg ctg 982  
 Ala His Phe Thr Val Gln Thr Val Asp Ala Gly Val Gly Glu Val Leu  
 280 285 290  
 gtc tac atc gag gac cct gaa ggc cac acc gag gag gct aag gtg gtt 1030  
 Val Tyr Ile Glu Asp Pro Glu Gly His Thr Glu Glu Ala Lys Val Val  
 295 300 305  
 ccc aac aat gac aag gat cgc acc tat gct gtc tcc tat gtg ccc aag 1078  
 Pro Asn Asn Asp Lys Asp Arg Thr Tyr Ala Val Ser Tyr Val Pro Lys  
 310 315 320  
 gtc gct ggg tta cac aag gtg acc gtg ctc ttt gct ggc cag aac att 1126  
 Val Ala Gly Leu His Lys Val Thr Val Leu Phe Ala Gly Gln Asn Ile  
 325 330 335

gaa cgc agt ccc ttt gag gtg aac gtg ggc atg gcc ctg gga gat gcc 1174  
 Glu Arg Ser Pro Phe Glu Val Asn Val Gly Met Ala Leu Gly Asp Ala  
 340 345 350 355  
 aac aag gtg tca gcc cgt ggc cct ggc ctg gaa cct gtg ggc aat gtg 1222  
 Asn Lys Val Ser Ala Arg Gly Pro Gly Leu Glu Pro Val Gly Asn Val  
 360 365 370  
 gcc aac aaa ccc acc tac ttt gac atc tac act gcg ggg gcc ggc act 1270  
 Ala Asn Lys Pro Thr Tyr Phe Asp Ile Tyr Thr Ala Gly Ala Gly Thr  
 375 380 385  
 ggc gat gtt gct gtg gtg atc gtg gac cca cag ggc cgg cgg gac aca 1318  
 Gly Asp Val Ala Val Val Ile Val Asp Pro Gln Gly Arg Arg Asp Thr  
 390 395 400  
 gtg gag gtg gcc ctg gag gac aag ggt gac agc acg ttc cgc tgc aca 1366  
 Val Glu Val Ala Leu Glu Asp Lys Gly Asp Ser Thr Phe Arg Cys Thr  
 405 410 415  
 tac aga cct gcc atg gag ggg cca cat acc gtg cat gtg gcc ttt gcg 1414  
 Tyr Arg Pro Ala Met Glu Gly Pro His Thr Val His Val Ala Phe Ala  
 420 425 430 435  
 ggt gcc ccc atc acc cgc agt ccc ttc cct gtc cat gtg tcg gaa gcc 1462  
 Gly Ala Pro Ile Thr Arg Ser Pro Phe Pro Val His Val Ser Glu Ala  
 440 445 450  
 tgt aac ccc aac gcc tgc cgc gcc tct ggg cga ggc ctg cag ccc aag 1510  
 Cys Asn Pro Asn Ala Cys Arg Ala Ser Gly Arg Gly Leu Gln Pro Lys  
 455 460 465  
 ggt gtt cgc gtg aaa gag gtg gct gac ttc aag gtg ttt acc aag ggt 1558  
 Gly Val Arg Val Lys Glu Val Ala Asp Phe Lys Val Phe Thr Lys Gly  
 470 475 480

gcc ggc agc ggg gag ctc aag gtc acg gtc aag ggg cca aag ggc aca 1606  
 Ala Gly Ser Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Thr  
 485 490 495  
 gag gag cca gtg aag gtg cgg gag gct ggg gat ggt gtg ttc gag tgc 1654  
 Glu Glu Pro Val Lys Val Arg Glu Ala Gly Asp Gly Val Phe Glu Cys  
 500 505 510 515  
 gag tac tac ccg gtg gtg cct ggg aag tat gtg gtg acc atc acg tgg 1702  
 Glu Tyr Tyr Pro Val Val Pro Gly Lys Tyr Val Val Thr Ile Thr Trp  
 520 525 530  
 ggc ggc tac gcc atc cct cgc agc ccc ttt gag gta cag gtg agc cca 1750  
 Gly Gly Tyr Ala Ile Pro Arg Ser Pro Phe Glu Val Gln Val Ser Pro  
 535 540 545  
 gag gca gga gtg caa aag gtc cgg gcc tgg ggt cct ggt ttg gag act 1798  
 Glu Ala Gly Val Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Thr  
 550 555 560  
 ggc cag gtg ggc aag tca gcc gat ttt gtg gtg gaa gcc att ggc acc 1846  
 Gly Gln Val Gly Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Thr  
 565 570 575  
 gag gtg ggg aca ctg ggc ttc tcc atc gag ggg ccc tca caa gcc aag 1894  
 Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser Gln Ala Lys  
 580 585 590 595  
 atc gaa tgt gac gat aag ggg gat ggc tcc tgc gat gtg cgg tac tgg 1942  
 Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp  
 600 605 610  
 ccc acg gag cct ggg gag tac gct gtg cac gtc atc tgt gac gat gag 1990  
 Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys Asp Asp Glu

615 620 625  
gac atc cga gac tca ccc ttc att gcc cac atc ctg ccc gcc cca cct 2038  
Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro Ala Pro Pro  
630 635 640  
gac tgc ttc cca gat aag gtg aag gcc ttt ggg cct ggc ctg gag cct 2086  
Asp Cys Phe Pro Asp Lys Val Lys Ala Phe Gly Pro Gly Leu Glu Pro  
645 650 655  
acc ggc tgc atc gtc gac aag ccc gct gag ttc acc att gat gct cgt 2134  
Thr Gly Cys Ile Val Asp Lys Pro Ala Glu Phe Thr Ile Asp Ala Arg  
660 665 670 675  
gca gct ggc aag gga gac ctg aag ctc tat gcc cag gac gcc gac ggc 2182  
Ala Ala Gly Lys Gly Asp Leu Lys Leu Tyr Ala Gln Asp Ala Asp Gly  
680 685 690  
tgt ccc atc gac atc aag gtg atc ccc aac ggc aac ggc acc ttc cgc 2230  
Cys Pro Ile Asp Ile Lys Val Ile Pro Asn Gly Asn Gly Thr Phe Arg  
695 700 705  
tgc tcc tac gtg ccc acc aag ccc att aag cac acc atc atc atc tcc 2278  
Cys Ser Tyr Val Pro Thr Lys Pro Ile Lys His Thr Ile Ile Ile Ser  
710 715 720  
tgg gga ggc gta aac gtg ccc aag agc ccc ttc cgg gtg aac gtg ggc 2326  
Trp Gly Gly Val Asn Val Pro Lys Ser Pro Phe Arg Val Asn Val Gly  
725 730 735  
gag ggc agc cac ccc gag cgg gta aag gtg tac ggc ccc gga gtg gag 2374  
Glu Gly Ser His Pro Glu Arg Val Lys Val Tyr Gly Pro Gly Val Glu  
740 745 750 755  
aag aca ggc ctc aag gcc aat gag ccc acc tac ttc acg gtg gac tgc 2422  
Lys Thr Gly Leu Lys Ala Asn Glu Pro Thr Tyr Phe Thr Val Asp Cys

760	765	770	
agc gag gcg ggg caa ggc gac gtg agc atc ggc atc aag tgc gcc cca	2470		
Ser Glu Ala Gly Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro			
775	780	785	
ggc gtg gig ggc cct gca gag gct gac att gac ttc gac atc atc aag	2518		
Gly Val Val Gly Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Ile Lys			
790	795	800	
aat gac aac gac acc ttc acc gtc aag tac acg cca cca ggg gcg ggc	2566		
Asn Asp Asn Asp Thr Phe Thr Val Lys Tyr Thr Pro Pro Gly Ala Gly			
805	810	815	
cgc tac acc atc atg gtg ctg ttt gcc aac cag gag atc ccc gcc agc	2614		
Arg Tyr Thr Ile Met Val Leu Phe Ala Asn Gln Glu Ile Pro Ala Ser			
820	825	830	835
ccc ttc cac atc aag gtg gac cca tcc cac gat gcc agc aaa gtc aag	2662		
Pro Phe His Ile Lys Val Asp Pro Ser His Asp Ala Ser Lys Val Lys			
840	845	850	
gcc gag ggc cct ggg ctg aat cgc aca ggt gtg gaa gtc ggg aag ccc	2710		
Ala Glu Gly Pro Gly Leu Asn Arg Thr Gly Val Glu Val Gly Lys Pro			
855	860	865	
acc cac ttc acg gtg ctg acc aag gga gcc ggc aag gcc aag ctg gat	2758		
Thr His Phe Thr Val Leu Thr Lys Gly Ala Gly Lys Ala Lys Leu Asp			
870	875	880	
gtg cag ttt gca ggg aca gcc aag ggc gag gtt gtg cgg gac ttt gag	2806		
Val Gln Phe Ala Gly Thr Ala Lys Gly Glu Val Val Arg Asp Phe Glu			
885	890	895	
atc ata gac aac cat gac tac tcc tac act gtc aag tac acc gct gtc	2854		

Ile Ile Asp Asn His Asp Tyr Ser Tyr Thr Val Lys Tyr Thr Ala Val  
 900 905 910 915  
 cag cag ggc aac atg gca gtg aca gtg act tat ggc ggg gac cct gtc 2902  
 Gln Gln Gly Asn Met Ala Val Thr Val Thr Tyr Gly Gly Asp Pro Val  
 920 925 930  
 ccc aag agc ccc ttt gtg gtg aat gig gca ccc ccg ctg gac ctc agc 2950  
 Pro Lys Ser Pro Phe Val Val Asn Val Ala Pro Pro Leu Asp Leu Ser  
 935 940 945  
 aaa atc aaa gtt cag ggc ctt aat agc aag gtg gct gtg gga cag gaa 2998  
 Lys Ile Lys Val Gln Gly Leu Asn Ser Lys Val Ala Val Gly Gln Glu  
 950 955 960  
 caa gca ttc tct gtg aac aca cga ggg gct ggc ggt cag ggc caa ctg 3046  
 Gln Ala Phe Ser Val Asn Thr Arg Gly Ala Gly Gly Gln Gly Gln Leu  
 965 970 975  
 gat gtg cgg atg act tcg ccc tct cgc cgg ccc atc ccc tgc aag ctg 3094  
 Asp Val Arg Met Thr Ser Pro Ser Arg Arg Pro Ile Pro Cys Lys Leu  
 980 985 990 995  
 gag cca ggc ggt gga gcg gaa gcc cag gct gtg cgc tac atg ccc ccg 3142  
 Glu Pro Gly Gly Gly Ala Glu Ala Gln Ala Val Arg Tyr Met Pro Pro  
 1000 1005 1010  
 gag gag ggg ccc tac aag gtg gat atc acc tac gat ggt cac ccg gtg 3190  
 Glu Glu Gly Pro Tyr Lys Val Asp Ile Thr Tyr Asp Gly His Pro Val  
 1015 1020 1025  
 cct ggc agc ccg ttt gct gtg gag ggt gtc ctg ccc cct gat ccc tcc 3238  
 Pro Gly Ser Pro Phe Ala Val Glu Gly Val Leu Pro Pro Asp Pro Ser  
 1030 1035 1040  
 aag gtc tgt gct tat ggc ccg ggt ctc aag ggt gga ctg gta ggc acc 3286



Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu Val Gly Thr  
 1045 1050 1055  
 ccc gcg cca ttc tcc atc gac acc aag ggg gct ggc aca ggt ggc ctg 3334  
 Pro Ala Pro Phe Ser Ile Asp Thr Lys Gly Ala Gly Thr Gly Gly Leu  
 1060 1065 1070 1075  
 ggg ctg acc gta gag ggc ccc tgc gag gcc aag atc gag tgc cag gac 3382  
 Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Lys Ile Glu Cys Gln Asp  
 1080 1085 1090  
 aat ggt gat ggc tca tgt gct gtc agc tac ctg ccc acg gag cct ggc 3430  
 Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr Glu Pro Gly  
 1095 1100 1105  
 gag tac acc atc aac atc ctg ttt gct gag gcc cac atc cct ggc tcg 3478  
 Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile Pro Gly Ser  
 1110 1115 1120  
 ccc ttc aaa gcc acc att cgg cct gtg ttt gac ccg agc aag gtg cgg 3526  
 Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser Lys Val Arg  
 1125 1130 1135  
 gcc agt gga ccg ggc ctg gag cgc ggc aag gtc ggt gag gca gcc acc 3574  
 Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu Ala Ala Thr  
 1140 1145 1150 1155  
 ttc act gtg gac tgc tca gag gca ggc gag gcg gag ctg acc att gag 3622  
 Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu Thr Ile Glu  
 1160 1165 1170  
 atc ctg tcg gat gcc ggg gtc aag gcc gag gtg ctg atc cac aac aac 3670  
 Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile His Asn Asn  
 1175 1180 1185

gcg gat ggc acc tac cac atc acc tac agc cct gcc ttc cct ggc acc 3718  
 Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe Pro Gly Thr  
 1190 1195 1200  
 tac acc att acc atc aag tat ggc ggg cat ccc gtg ccc aaa ttc ccc 3766  
 Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro Lys Phe Pro  
 1205 1210 1215  
 acc cgt gtc cat gtg cag cct gcg gtc gat acc agt ggc gtc aag gtc 3814  
 Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly Val Lys Val  
 1220 1225 1230 1235  
 tca ggg cct ggt gtt gag cca cac ggt gtc ctg cgg gag gtg acc act 3862  
 Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu Val Thr Thr  
 1240 1245 1250  
 gag ttc act gtg gat gca aga tcc cta aca gcc aca ggc ggc aac cac 3910  
 Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly Gly Asn His  
 1255 1260 1265  
 gtg acg gct cgt gtg ctc aac ccc tcg ggg gcc aag aca gac acc tat 3958  
 Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr Asp Thr Tyr  
 1270 1275 1280  
 glg aca gac aat ggg gac ggc acc tac cga gtg cag tac acc gcc tac 4006  
 Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr Thr Ala Tyr  
 1285 1290 1295  
 gag gag ggc gtg cat ctg gtg gag gtc ctg tat gat gag gtc gct gtg 4054  
 Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu Val Ala Val  
 1300 1305 1310 1315  
 ccc aag agc ccc ttc cga gtg ggc gtg acc gag ggc tgt gat ccc acc 4102  
 Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys Asp Pro Thr  
 1320 1325 1330

cgc gtc cga gcc ttc ggg cca ggc ctg gag ggt ggc ttg gtc aac aag 4150  
 Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu Val Asn Lys  
 1335 1340 1345  
 gcc aac cga ttc act gtg gag acc agg gga gcg ggc acc ggg ggc ctt 4198  
 Ala Asn Arg Phe Thr Val Glu Thr Arg Gly Ala Gly Thr Gly Gly Leu  
 1350 1355 1360  
 ggc cta gcc atc gag ggt ccc tcg gaa gcc aag atg tcc tgc aag gac 4246  
 Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser Cys Lys Asp  
 1365 1370 1375  
 aac aag gat ggt agc tgc acc gtg gag tac atc ccc ttc act cct gga 4294  
 Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe Thr Pro Gly  
 1380 1385 1390 1395  
 gac tat gac gtc aac atc acc ttc ggg ggg cgg ccc atc cca ggg agc 4342  
 Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile Pro Gly Ser  
 1400 1405 1410  
 ccg ttc cgc gtg cca gtg aag gat gtg gtg gac cct ggg aag gtg aag 4390  
 Pro Phe Arg Val Pro Val Lys Asp Val Val Asp Pro Gly Lys Val Lys  
 1415 1420 1425  
 tgc tca ggg cca ggg ctg ggg gct ggt gtc agg gcc cgg gtt cct cag 4438  
 Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg Val Pro Gln  
 1430 1435 1440  
 acc ttc aca gtg gac tgc agt caa gct ggc cgg gcg ccc ctg cag gtg 4486  
 Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro Leu Gln Val  
 1445 1450 1455  
 gct gtg ctg ggc ccc aca ggt gtg gcc gag cct gtg gag gtg cgg gac 4534  
 Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu Val Arg Asp

1460	1465	1470	1475	
aat gga gat ggc acc cac act gtc cac tac acc cca gcc act gac ggg				4582
Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala Thr Asp Gly				
	1480	1485	1490	
ccc tac acg gta gcc gtc aag tat gct gac cag gag gtg cca cgc agc				4630
Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val Pro Arg Ser				
	1495	1500	1505	
ccc ttc aag atc aag gtc ctc cca gct cat gat gcc agc aag gtg cgg				4678
Pro Phe Lys Ile Lys Val Leu Pro Ala His Asp Ala Ser Lys Val Arg				
	1510	1515	1520	
gcc agc ggg cca ggc ctc aac gcc tct ggc atc cct gcc agc ctg cct				4726
Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala Ser Leu Pro				
	1525	1530	1535	
gtg gag ttc acc atc gac gca cgg gac gcg ggc gag ggg ttg ctc act				4774
Val Glu Phe Thr Ile Asp Ala Arg Asp Ala Gly Glu Gly Leu Leu Thr				
1540	1545	1550	1555	
gtc cag atc ttg ggc ccc gag ggt aag ccc aag aag gcc aac atc cgg				4822
Val Gln Ile Leu Gly Pro Glu Gly Lys Pro Lys Lys Ala Asn Ile Arg				
	1560	1565	1570	
gac aat ggg gat ggc acg tac gct gtg tcc tac ctg ccg gac atg agt				4870
Asp Asn Gly Asp Gly Thr Tyr Ala Val Ser Tyr Leu Pro Asp Met Ser				
	1575	1580	1585	
ggc cgg tac acc atc acc atc aag tat ggc ggt gat gag atc ccc tac				4918
Gly Arg Tyr Thr Ile Thr Ile Lys Tyr Gly Gly Asp Glu Ile Pro Tyr				
	1590	1595	1600	
tcg ccc ttc cgc atc cat gct ctg ccc act ggg gat gcc agc aag tgc				4966
Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala Ser Lys Cys				

1605	1610	1615	
ctc gtc aca gtg tcc att gga ggc cat ggc ctg ggt gcc tgc ctg ggc	5014		
Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala Cys Leu Gly			
1620	1625	1630	1635
cct cga atc cag att ggg cag gag acg gtg atc acg gtg gat gcc aag	5062		
Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val Asp Ala Lys			
1640	1645	1650	
gca gcc ggt gag ggg aag gtg aca tgc acg gtg tcc acg ccg gat ggc	5110		
Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr Pro Asp Gly			
1655	1660	1665	
gca gag ctc gat gtg gat gtg gtt gag aac cat gac ggt acc ttt gac	5158		
Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly Thr Phe Asp			
1670	1675	1680	
atc tac tac aca gcg ccc gag ccg ggc aag tac gtc atc acc atc cgc	5206		
Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile Thr Ile Arg			
1685	1690	1695	
ttc ggg ggt gag cac atc ccc aac agc ccc ttc cac gtg ctg gcg tgt	5254		
Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val Leu Ala Cys			
1700	1705	1710	1715
gac ccc ctg ccg cac gag gag gag ccc tct gaa gtg cca cag ctg cgc	5302		
Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro Gln Leu Arg			
1720	1725	1730	
cag ccc tac gct cct ccc cgg ccc ggc gcc cgc ccc aca cac tgg gcc	5350		
Gln Pro Tyr Ala Pro Pro Arg Pro Gly Ala Arg Pro Thr His Trp Ala			
1735	1740	1745	
aca gag gag cca gtg gtg cct gtg gag cca atg gag tcc atg ctg agg	5398		

Thr Glu Glu Pro Val Val Pro Val Glu Pro Met Glu Ser Met Leu Arg  
 1750 1755 1760  
 ccc ttc aac ctg gtc atc ccc ttc gcg gtg cag aaa ggg gag ctc aca 5446  
 Pro Phe Asn Leu Val Ile Pro Phe Ala Val Gln Lys Gly Glu Leu Thr  
 1765 1770 1775  
 gga gag gtg cgg atg ccc tcg ggg aag acg gca cgg ccc aac atc acc 5494  
 Gly Glu Val Arg Met Pro Ser Gly Lys Thr Ala Arg Pro Asn Ile Thr  
 1780 1785 1790 1795  
 gac aac aag gac ggc acc atc acg gtg agg tat gca ccc act gag aaa 5542  
 Asp Asn Lys Asp Gly Thr Ile Thr Val Arg Tyr Ala Pro Thr Glu Lys  
 1800 1805 1810  
 ggc ctg cac cag atg ggg atc aag tat gac ggc aac cac atc cct ggg 5590  
 Gly Leu His Gln Met Gly Ile Lys Tyr Asp Gly Asn His Ile Pro Gly  
 1815 1820 1825  
 agc ccc tta cag ttc tat gtg gat gcc atc aac agc cgc cat gtc agt 5638  
 Ser Pro Leu Gln Phe Tyr Val Asp Ala Ile Asn Ser Arg His Val Ser  
 1830 1835 1840  
 gcc tat ggg cca ggc ctg agc cat ggc atg gtc aac aag cca gcc acc 5686  
 Ala Tyr Gly Pro Gly Leu Ser His Gly Met Val Asn Lys Pro Ala Thr  
 1845 1850 1855  
 ttc act att gtc acc aaa gat gct gga gaa ggg ggt ctg tca ctg gcc 5734  
 Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala  
 1860 1865 1870 1875  
 gtg gag ggc cca tcc aag gca gag atc acc tgt aag gac aac aag gat 5782  
 Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp Asn Lys Asp  
 1880 1885 1890  
 ggc acc tgc acc gtg tcc tat ctg ccg act gcg cct gga gac tac agc 5830

Gly Thr Cys Thr Val Ser Tyr Leu Pro Thr Ala Pro Gly Asp Tyr Ser  
 1895 1900 1905  
 atc atc gtg cgc ttc gat gac aag cac atc ccg ggg agc ccc ttc aca 5878  
 Ile Ile Val Arg Phe Asp Asp Lys His Ile Pro Gly Ser Pro Phe Thr  
 1910 1915 1920  
 gcc aag atc aca ggt gat gac tcc atg agg acc tca cag ctg aat gtg 5926  
 Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln Leu Asn Val  
 1925 1930 1935  
 ggc acc tcc acg gac gtg tca ctg aag atc acc gag agt gat ctg agc 5974  
 Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser Asp Leu Ser  
 1940 1945 1950 1955  
 cag ctg acc gcc agc atc cgt gcc ccc tcg ggc aac gag gag ccc tgc 6022  
 Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu Glu Pro Cys  
 1960 1965 1970  
 ctg ctg aag cgc ctg ccc aac cgg cac att ggg atc tcc ttc acc ccc 6070  
 Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser Phe Thr Pro  
 1975 1980 1985  
 aag gag gtc ggg gag cac gtg gtg agc gtg cgc aag agt ggc aag cat 6118  
 Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser Gly Lys His  
 1990 1995 2000  
 gtc acc aac agc ccc ttc aag atc ctg gtg ggg cca tct gag atc ggg 6166  
 Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser Glu Ile Gly  
 2005 2010 2015  
 gac gcc agc aag gtg cgg gtc tgg ggc aag ggg ctt tcc gag gga cac 6214  
 Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser Glu Gly His  
 2020 2025 2030 2035

aca ttc cag gtg gca gag ttc atc gtg gac act cgc aat gca ggt tat 6262  
 Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn Ala Gly Tyr  
 2040 2045 2050  
 ggg ggc ttg ggg ctg agt att gaa ggc cca agc aag glg gac atc aac 6310  
 Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn  
 2055 2060 2065  
 tgt gag gac atg gag gac ggg aca tgc aaa gtc acc tac tgc ccc acc 6358  
 Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr Cys Pro Thr  
 2070 2075 2080  
 gag ccc ggc acc tac atc atc aac atc aag ttt gct gac aag cac glg 6406  
 Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp Lys His Val  
 2085 2090 2095  
 cct gga agc ccc ttc act gtg aag gtg acc ggc gag ggc cgc atg aag 6454  
 Pro Gly Ser Pro Phe Thr Val Lys Val Thr Gly Glu Gly Arg Met Lys  
 2100 2105 2110 2115  
 gag agc atc acc cgg cgg aga cag gca cct tcc atc gcc acc atc ggc 6502  
 Glu Ser Ile Thr Arg Arg Arg Gln Ala Pro Ser Ile Ala Thr Ile Gly  
 2120 2125 2130  
 agc acc tgt gac ctc aac ctc aag atc cca gga aac tgg ttc cag atg 6550  
 Ser Thr Cys Asp Leu Asn Leu Lys Ile Pro Gly Asn Trp Phe Gln Met  
 2135 2140 2145  
 gtg tct gcc cag gag cgc ctg aca cgc acc ttc aca cgc agc agc cac 6598  
 Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg Ser Ser His  
 2150 2155 2160  
 acc tac acc cgc acg gag cgc acg gag atc agc aag acg cgg ggc ggg 6646  
 Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr Arg Gly Gly  
 2165 2170 2175



gag aca aag ccc gag glg cgg glg gag gag tcc acc cag gtc ggc ggg 6694  
 Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln Val Gly Gly  
 2180 2185 2190 2195  
 gac ccc ttc cct gct gtg ttt ggg gac ttc ctg ggc cgg gag cgc ctg 6742  
 Asp Pro Phe Pro Ala Val Phe Gly Asp Phe Leu Gly Arg Glu Arg Leu  
 2200 2205 2210  
 gga tcc ttc ggc agc atc acc cgg cag cag gag ggt gag gcc agc tct 6790  
 Gly Ser Phe Gly Ser Ile Thr Arg Gln Gln Glu Gly Glu Ala Ser Ser  
 2215 2220 2225  
 cag gac atg act gca cag gtg acc agc cca tcg ggc aag gtg gaa gcc 6838  
 Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys Val Glu Ala  
 2230 2235 2240  
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 Pro Gln Glu Met Gly Pro His Thr Val Ala Val Lys Tyr Arg Gly Gln  
 2260 2265 2270 2275  
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 His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu  
 2280 2285 2290  
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 Gly Gly Ala His Lys Val Arg Ala Gly Arg Ala Gly Leu Glu Arg Gly  
 2295 2300 2305  
 gtg gcc ggc gtg cca gcc gag ttc agc atc tgg acc cgg gag gct ggc 7078  
 Val Ala Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly

2310	2315	2320	
gct ggg ggc ctg tcc att gct gtc gag ggt cct agc aaa gcg gag att			7126
Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile			
2325	2330	2335	
gca ttt gag gat cgc aaa gat ggc tcc tgc ggc gtc tcc tat gtc gtc			7174
Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser Tyr Val Val			
2340	2345	2350	2355
cag gaa cca ggt gac tat gag gtc tcc atc aag ttc aat gat gag cac			7222
Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn Asp Glu His			
2360	2365	2370	
atc cca gac agc ccc ttt gtg gtg cct gtg gcc tcc ctc tcg gat gac			7270
Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu Ser Asp Asp			
2375	2380	2385	
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Ala Arg Arg Leu Thr Val Thr Ser Leu Gln Glu Thr Gly Leu Lys Val			
2390	2395	2400	
aac cag cca gcg tcc ttt gcc gtg cag ctg aac ggt gcc cgg ggc gtg			7366
Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala Arg Gly Val			
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att gat gcc cgg gtg cac aca ccc tcg ggg gct gtg gag gag tgc tac			7414
Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu Glu Cys Tyr			
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gtc tct gag ctg gac agt gac aag cac acc atc cgc ttc atc ccc cac			7462
Val Ser Glu Leu Asp Ser Asp Lys His Thr Ile Arg Phe Ile Pro His			
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Glu Asn Gly Val His Ser Ile Asp Val Lys Phe Asn Gly Ala His Ile			

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cct gga agt ccc ttc aag atc cgc gtt ggg gag cag agc cag gct ggg	7558		
Pro Gly Ser Pro Phe Lys Ile Arg Val Gly Glu Gln Ser Gln Ala Gly			
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gac cca ggc ttg gtg tca gcc tac ggt cct ggg ctc gag gga ggc act	7606		
Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu Gly Gly Thr			
2485	2490	2495	
acc ggt gtg tca tca gag ttc atc gtg aac acc ctg aat gcc ggc tcg	7654		
Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn Ala Gly Ser			
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ggg gcc ttg tct gtc acc att gat ggc ccc tcc aag gtg cag ctg gac	7702		
Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val Gln Leu Asp			
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Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr Pro Met Ala			
2535	2540	2545	
cct ggc aac tac ctc att gcc atc aag tac ggt ggc ccc cag cac atc	7798		
Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro Gln His Ile			
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gtg ggc agc ccc ttc aag gcc aag gtc act ggt ccg agg ctg tcc gga	7846		
Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg Leu Ser Gly			
2565	2570	2575	
ggc cac agc ctt cac gaa aca tcc acg gtt ctg gtg gag act gtg acc	7894		
Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu Thr Val Thr			
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Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile Pro Lys Phe  
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 Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys Ser Lys Ala  
 2630 2635 2640  
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 Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys Thr Pro Cys  
 2645 2650 2655  
 gag gag gtg tac gtg aag cac atg ggg aac cgg gtg tac aat gtc acc 8134  
 Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr Asn Val Thr  
 2660 2665 2670 2675  
 tac act gtc aag gag aaa ggg gac tac atc ctc att gtc aag tgg ggt 8182  
 Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val Lys Trp Gly  
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 Asp Glu Ser Val Pro Gly Ser Pro Phe Lys Val Lys Val Pro  
 2695 2700 2705  
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 aactccaaat aaagtgcgcc tgcgcc 8971

<210> 44

<211> 2705

<212> PRT

<213> Homo sapiens

<400> 44

Met Pro Ser Thr Glu Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys

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Ile Gln Gln Asn Thr Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys

20 25 30

Val Gly Lys Arg Leu Thr Asp Leu Gln Arg Asp Leu Ser Asp Gly Leu

35 40 45

Arg Leu Ile Ala Leu Leu Glu Val Leu Ser Gln Lys Arg Met Tyr Arg

50 55 60

Lys Phe His Pro Arg Pro Asn Phe Arg Gln Met Lys Leu Glu Asn Val

65 70 75 80

Ser Val Ala Leu Glu Phe Leu Glu Arg Glu His Ile Lys Leu Val Ser

85 90 95

Ile Asp Ser Lys Ala Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly

100 105 110

Leu Ile Trp Thr Leu Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp

115	120	125	
Glu Asp Glu Asp Asp Glu Asp Ala Arg Lys Gln Thr Pro Lys Gln Arg			
130	135	140	
Leu Leu Gly Trp Ile Gln Asn Lys Val Pro Gln Leu Pro Ile Thr Asn			
145	150	155	160
Phe Asn Arg Asp Trp Gln Asp Gly Lys Ala Leu Gly Ala Leu Val Asp			
165	170	175	
Asn Cys Ala Pro Gly Leu Cys Pro Asp Trp Glu Ala Trp Asp Pro Asn			
180	185	190	
Gln Pro Val Glu Asn Ser Arg Glu Ala Met Gln Gln Ala Asp Asp Trp			
195	200	205	
Leu Gly Val Pro Gln Val Ile Ala Pro Glu Glu Ile Val Asp Pro Asn			
210	215	220	
Val Asp Glu His Ser Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala			
225	230	235	240
Lys Leu Lys Pro Gly Ala Pro Val Arg Ser Lys Gln Leu Asn Pro Lys			
245	250	255	
Lys Ala Ile Ala Tyr Gly Pro Gly Ile Glu Pro Gln Gly Asn Thr Val			
260	265	270	
Leu Gln Pro Ala His Phe Thr Val Gln Thr Val Asp Ala Gly Val Gly			
275	280	285	
Glu Val Leu Val Tyr Ile Glu Asp Pro Glu Gly His Thr Glu Glu Ala			
290	295	300	
Lys Val Val Pro Asn Asn Asp Lys Asp Arg Thr Tyr Ala Val Ser Tyr			
305	310	315	320
Val Pro Lys Val Ala Gly Leu His Lys Val Thr Val Leu Phe Ala Gly			

325 330 335  
Gln Asn Ile Glu Arg Ser Pro Phe Glu Val Asn Val Gly Met Ala Leu  
340 345 350  
Gly Asp Ala Asn Lys Val Ser Ala Arg Gly Pro Gly Leu Glu Pro Val  
355 360 365  
Gly Asn Val Ala Asn Lys Pro Thr Tyr Phe Asp Ile Tyr Thr Ala Gly  
370 375 380  
Ala Gly Thr Gly Asp Val Ala Val Val Ile Val Asp Pro Gln Gly Arg  
385 390 395 400  
Arg Asp Thr Val Glu Val Ala Leu Glu Asp Lys Gly Asp Ser Thr Phe  
405 410 415  
Arg Cys Thr Tyr Arg Pro Ala Met Glu Gly Pro His Thr Val His Val  
420 425 430  
Ala Phe Ala Gly Ala Pro Ile Thr Arg Ser Pro Phe Pro Val His Val  
435 440 445  
Ser Glu Ala Cys Asn Pro Asn Ala Cys Arg Ala Ser Gly Arg Gly Leu  
450 455 460  
Gln Pro Lys Gly Val Arg Val Lys Glu Val Ala Asp Phe Lys Val Phe  
465 470 475 480  
Thr Lys Gly Ala Gly Ser Gly Glu Leu Lys Val Thr Val Lys Gly Pro  
485 490 495  
Lys Gly Thr Glu Glu Pro Val Lys Val Arg Glu Ala Gly Asp Gly Val  
500 505 510  
Phe Glu Cys Glu Tyr Tyr Pro Val Val Pro Gly Lys Tyr Val Val Thr  
515 520 525  
Ile Thr Trp Gly Gly Tyr Ala Ile Pro Arg Ser Pro Phe Glu Val Gln  
530 535 540

Val Ser Pro Glu Ala Gly Val Gln Lys Val Arg Ala Trp Gly Pro Gly  
545 550 555 560  
Leu Glu Thr Gly Gln Val Gly Lys Ser Ala Asp Phe Val Val Glu Ala  
565 570 575  
Ile Gly Thr Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser  
580 585 590  
Gln Ala Lys Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val  
595 600 605  
Arg Tyr Trp Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys  
610 615 620  
Asp Asp Glu Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro  
625 630 635 640  
Ala Pro Pro Asp Cys Phe Pro Asp Lys Val Lys Ala Phe Gly Pro Gly  
645 650 655  
Leu Glu Pro Thr Gly Cys Ile Val Asp Lys Pro Ala Glu Phe Thr Ile  
660 665 670  
Asp Ala Arg Ala Ala Gly Lys Gly Asp Leu Lys Leu Tyr Ala Gln Asp  
675 680 685  
Ala Asp Gly Cys Pro Ile Asp Ile Lys Val Ile Pro Asn Gly Asn Gly  
690 695 700  
Thr Phe Arg Cys Ser Tyr Val Pro Thr Lys Pro Ile Lys His Thr Ile  
705 710 715 720  
Ile Ile Ser Trp Gly Gly Val Asn Val Pro Lys Ser Pro Phe Arg Val  
725 730 735  
Asn Val Gly Glu Gly Ser His Pro Glu Arg Val Lys Val Tyr Gly Pro  
740 745 750



Gly Val Glu Lys Thr Gly Leu Lys Ala Asn Glu Pro Thr Tyr Phe Thr  
755 760 765

Val Asp Cys Ser Glu Ala Gly Gln Gly Asp Val Ser Ile Gly Ile Lys  
770 775 780

Cys Ala Pro Gly Val Val Gly Pro Ala Glu Ala Asp Ile Asp Phe Asp  
785 790 795 800

Ile Ile Lys Asn Asp Asn Asp Thr Phe Thr Val Lys Tyr Thr Pro Pro  
805 810 815

Gly Ala Gly Arg Tyr Thr Ile Met Val Leu Phe Ala Asn Gln Glu Ile  
820 825 830

Pro Ala Ser Pro Phe His Ile Lys Val Asp Pro Ser His Asp Ala Ser  
835 840 845

Lys Val Lys Ala Glu Gly Pro Gly Leu Asn Arg Thr Gly Val Glu Val  
850 855 860

Gly Lys Pro Thr His Phe Thr Val Leu Thr Lys Gly Ala Gly Lys Ala  
865 870 875 880

Lys Leu Asp Val Gln Phe Ala Gly Thr Ala Lys Gly Glu Val Val Arg  
885 890 895

Asp Phe Glu Ile Ile Asp Asn His Asp Tyr Ser Tyr Thr Val Lys Tyr  
900 905 910

Thr Ala Val Gln Gln Gly Asn Met Ala Val Thr Val Thr Tyr Gly Gly  
915 920 925

Asp Pro Val Pro Lys Ser Pro Phe Val Val Asn Val Ala Pro Pro Leu  
930 935 940

Asp Leu Ser Lys Ile Lys Val Gln Gly Leu Asn Ser Lys Val Ala Val  
945 950 955 960

Gly Gln Glu Gln Ala Phe Ser Val Asn Thr Arg Gly Ala Gly Gly Gln

965 970 975  
Gly Gln Leu Asp Val Arg Met Thr Ser Pro Ser Arg Arg Pro Ile Pro  
980 985 990  
Cys Lys Leu Glu Pro Gly Gly Gly Ala Glu Ala Gln Ala Val Arg Tyr  
995 1000 1005  
Met Pro Pro Glu Glu Gly Pro Tyr Lys Val Asp Ile Thr Tyr Asp Gly  
1010 1015 1020  
His Pro Val Pro Gly Ser Pro Phe Ala Val Glu Gly Val Leu Pro Pro  
1025 1030 1035 1040  
Asp Pro Ser Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu  
1045 1050 1055  
Val Gly Thr Pro Ala Pro Phe Ser Ile Asp Thr Lys Gly Ala Gly Thr  
1060 1065 1070  
Gly Gly Leu Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Lys Ile Glu  
1075 1080 1085  
Cys Gln Asp Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr  
1090 1095 1100  
Glu Pro Gly Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile  
1105 1110 1115 1120  
Pro Gly Ser Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser  
1125 1130 1135  
Lys Val Arg Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu  
1140 1145 1150  
Ala Ala Thr Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu  
1155 1160 1165  
Thr Ile Glu Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile

1170	1175	1180	
His Asn Asn Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe			
1185	1190	1195	1200
Pro Gly Thr Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro			
	1205	1210	1215
Lys Phe Pro Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly			
	1220	1225	1230
Val Lys Val Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu			
	1235	1240	1245
Val Thr Thr Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly			
	1250	1255	1260
Gly Asn His Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr			
1265	1270	1275	1280
Asp Thr Tyr Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr			
	1285	1290	1295
Thr Ala Tyr Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu			
	1300	1305	1310
Val Ala Val Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys			
	1315	1320	1325
Asp Pro Thr Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu			
	1330	1335	1340
Val Asn Lys Ala Asn Arg Phe Thr Val Glu Thr Arg Gly Ala Gly Thr			
1345	1350	1355	1360
Gly Gly Leu Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser			
	1365	1370	1375
Cys Lys Asp Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe			
	1380	1385	1390

Thr Pro Gly Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile  
 1395 1400 1405  
 Pro Gly Ser Pro Phe Arg Val Pro Val Lys Asp Val Val Asp Pro Gly  
 1410 1415 1420  
 Lys Val Lys Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg  
 1425 1430 1435 1440  
 Val Pro Gln Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro  
 1445 1450 1455  
 Leu Gln Val Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu  
 1460 1465 1470  
 Val Arg Asp Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala  
 1475 1480 1485  
 Thr Asp Gly Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val  
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 Pro Arg Ser Pro Phe Lys Ile Lys Val Leu Pro Ala His Asp Ala Ser  
 1505 1510 1515 1520  
 Lys Val Arg Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala  
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 Ser Leu Pro Val Glu Phe Thr Ile Asp Ala Arg Asp Ala Gly Glu Gly  
 1540 1545 1550  
 Leu Leu Thr Val Gln Ile Leu Gly Pro Glu Gly Lys Pro Lys Lys Ala  
 1555 1560 1565  
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 1570 1575 1580  
 Asp Met Ser Gly Arg Tyr Thr Ile Thr Ile Lys Tyr Gly Gly Asp Glu  
 1585 1590 1595 1600

Ile Pro Tyr Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala  
1605 1610 1615

Ser Lys Cys Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala  
1620 1625 1630

Cys Leu Gly Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val  
1635 1640 1645

Asp Ala Lys Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr  
1650 1655 1660

Pro Asp Gly Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly  
1665 1670 1675 1680

Thr Phe Asp Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile  
1685 1690 1695

Thr Ile Arg Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val  
1700 1705 1710

Leu Ala Cys Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro  
1715 1720 1725

Gln Leu Arg Gln Pro Tyr Ala Pro Pro Arg Pro Gly Ala Arg Pro Thr  
1730 1735 1740

His Trp Ala Thr Glu Glu Pro Val Val Pro Val Glu Pro Met Glu Ser  
1745 1750 1755 1760

Met Leu Arg Pro Phe Asn Leu Val Ile Pro Phe Ala Val Gln Lys Gly  
1765 1770 1775

Glu Leu Thr Gly Glu Val Arg Met Pro Ser Gly Lys Thr Ala Arg Pro  
1780 1785 1790

Asn Ile Thr Asp Asn Lys Asp Gly Thr Ile Thr Val Arg Tyr Ala Pro  
1795 1800 1805

Thr Glu Lys Gly Leu His Gln Met Gly Ile Lys Tyr Asp Gly Asn His

1810	1815	1820	
Ile Pro Gly Ser Pro Leu Gln Phe Tyr Val Asp Ala Ile Asn Ser Arg			
1825	1830	1835	1840
His Val Ser Ala Tyr Gly Pro Gly Leu Ser His Gly Met Val Asn Lys			
1845	1850	1855	
Pro Ala Thr Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu			
1860	1865	1870	
Ser Leu Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp			
1875	1880	1885	
Asn Lys Asp Gly Thr Cys Thr Val Ser Tyr Leu Pro Thr Ala Pro Gly			
1890	1895	1900	
Asp Tyr Ser Ile Ile Val Arg Phe Asp Asp Lys His Ile Pro Gly Ser			
1905	1910	1915	1920
Pro Phe Thr Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln			
1925	1930	1935	
Leu Asn Val Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser			
1940	1945	1950	
Asp Leu Ser Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu			
1955	1960	1965	
Glu Pro Cys Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser			
1970	1975	1980	
Phe Thr Pro Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser			
1985	1990	1995	2000
Gly Lys His Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser			
2005	2010	2015	
Glu Ile Gly Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser			

2020	2025	2030	
Glu Gly His Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn			
2035	2040	2045	
Ala Gly Tyr Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val			
2050	2055	2060	
Asp Ile Asn Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr			
2065	2070	2075	2080
Cys Pro Thr Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp			
2085	2090	2095	
Lys His Val Pro Gly Ser Pro Phe Thr Val Lys Val Thr Gly Glu Gly			
2100	2105	2110	
Arg Met Lys Glu Ser Ile Thr Arg Arg Arg Gln Ala Pro Ser Ile Ala			
2115	2120	2125	
Thr Ile Gly Ser Thr Cys Asp Leu Asn Leu Lys Ile Pro Gly Asn Trp			
2130	2135	2140	
Phe Gln Met Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg			
2145	2150	2155	2160
Ser Ser His Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr			
2165	2170	2175	
Arg Gly Gly Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln			
2180	2185	2190	
Val Gly Gly Asp Pro Phe Pro Ala Val Phe Gly Asp Phe Leu Gly Arg			
2195	2200	2205	
Glu Arg Leu Gly Ser Phe Gly Ser Ile Thr Arg Gln Gln Glu Gly Glu			
2210	2215	2220	
Ala Ser Ser Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys			
2225	2230	2235	2240

Val Glu Ala Ala Glu Ile Val Glu Gly Glu Asp Ser Ala Tyr Ser Val

2245

2250

2255

Arg Phe Val Pro Gln Glu Met Gly Pro His Thr Val Ala Val Lys Tyr

2260

2265

2270

Arg Gly Gln His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro

2275

2280

2285

Leu Gly Glu Gly Gly Ala His Lys Val Arg Ala Gly Arg Ala Gly Leu

2290

2295

2300

Glu Arg Gly Val Ala Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg

2305

2310

2315

2320

Glu Ala Gly Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys

2325

2330

2335

Ala Glu Ile Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser

2340

2345

2350

Tyr Val Val Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn

2355

2360

2365

Asp Glu His Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu

2370

2375

2380

Ser Asp Asp Ala Arg Arg Leu Thr Val Thr Ser Leu Gln Glu Thr Gly

2385

2390

2395

2400

Leu Lys Val Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala

2405

2410

2415

Arg Gly Val Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu

2420

2425

2430

Glu Cys Tyr Val Ser Glu Leu Asp Ser Asp Lys His Thr Ile Arg Phe

2435

2440

2445



Ile Pro His Glu Asn Gly Val His Ser Ile Asp Val Lys Phe Asn Gly

2450

2455

2460

Ala His Ile Pro Gly Ser Pro Phe Lys Ile Arg Val Gly Glu Gln Ser

2465

2470

2475

2480

Gln Ala Gly Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu

2485

2490

2495

Gly Gly Thr Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn

2500

2505

2510

Ala Gly Ser Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val

2515

2520

2525

Gln Leu Asp Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr

2530

2535

2540

Pro Met Ala Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro

2545

2550

2555

2560

Gln His Ile Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg

2565

2570

2575

Leu Ser Gly Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu

2580

2585

2590

Thr Val Thr Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile

2595

2600

2605

Pro Lys Phe Ser Ser Asp Ala Ser Lys Val Val Thr Arg Gly Pro Gly

2610

2615

2620

Leu Ser Gln Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys

2625

2630

2635

2640

Ser Lys Ala Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys

2645

2650

2655

Thr Pro Cys Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr

2660 2665 2670  
 Asn Val Thr Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val

2675 2680 2685  
 Lys Trp Gly Asp Glu Ser Val Pro Gly Ser Pro Phe Lys Val Lys Val

2690 2695 2700

Pro

2705

<210> 45

<211> 2016

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210).. (1352)

<400> 45

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 gaccccgctg cgcacggcct gtccgctgca caccagcttg ttggcgcttt cgtcgccgcg 180  
 ctgcgcccg gctactcctg cgcgccaca atg agc tcc cgc atc gcc agg gcg 233

Met Ser Ser Arg Ile Ala Arg Ala

1

5

ctc gcc tta gtc gtc acc ctt ctc cac ttg acc agg ctg gcg ctc tcc 281

Leu Ala Leu Val Val Thr Leu Leu His Leu Thr Arg Leu Ala Leu Ser

10

15

20

acc tgc ccc gct gcc tgc cac tgc ccc ctg gag gcg ccc aag tgc gcg 329

Thr Cys Pro Ala Ala Cys His Cys Pro Leu Glu Ala Pro Lys Cys Ala

25	30	35	40	
ccg gga gtc ggg ctg gtc cgg gac ggc tgc ggc tgc tgt aag gtc tgc	377			
Pro Gly Val Gly Leu Val Arg Asp Gly Cys Gly Cys Cys Lys Val Cys				
45	50	55		
gcc aag cag ctc aac gag gac tgc agc aaa acg cag ccc tgc gac cac	425			
Ala Lys Gln Leu Asn Glu Asp Cys Ser Lys Thr Gln Pro Cys Asp His				
60	65	70		
acc aag ggg ctg gaa tgc aac ttc ggc gcc agc tcc acc gct ctg aag	473			
Thr Lys Gly Leu Glu Cys Asn Phe Gly Ala Ser Ser Thr Ala Leu Lys				
75	80	85		
ggg atc tgc aga gct cag tca gag ggc aga ccc tgt gaa tat aac tcc	521			
Gly Ile Cys Arg Ala Gln Ser Glu Gly Arg Pro Cys Glu Tyr Asn Ser				
90	95	100		
aga atc tac caa aac ggg gaa agt ttc cag ccc aac tgt aaa cat cag	569			
Arg Ile Tyr Gln Asn Gly Glu Ser Phe Gln Pro Asn Cys Lys His Gln				
105	110	115	120	
tgc aca tgt att gat ggc gcc gtg ggc tgc att cct ctg tgt ccc caa	617			
Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Ile Pro Leu Cys Pro Gln				
125	130	135		
gaa cta tct ctc ccc aac ttg ggc tgt ccc aac cct cgg ctg gtc aaa	665			
Glu Leu Ser Leu Pro Asn Leu Gly Cys Pro Asn Pro Arg Leu Val Lys				
140	145	150		
gtt acc ggg cag tgc tgc gag gag tgg gtc tgt gac gag gat agt atc	713			
Val Thr Gly Gln Cys Cys Glu Glu Trp Val Cys Asp Glu Asp Ser Ile				
155	160	165		
aag gac ccc atg gag gac cag gac ggc ctc ctt ggc aag gag ctg gga	761			

Lys Asp Pro Met Glu Asp Gln Asp Gly Leu Leu Gly Lys Glu Leu Gly  
 170 175 180  
 ttc gat gcc tcc gag gtg gag ttg acg aga aac aat gaa ttg att gca 809  
 Phe Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn Glu Leu Ile Ala  
 185 190 195 200  
 gtt gga aaa ggc agc tca ctg aag cgg ctc cct gtt ttt gga atg gag 857  
 Val Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val Phe Gly Met Glu  
 205 210 215  
 cct cgc atc cta tac aac cct tta caa ggc cag aaa tgt att gtt caa 905  
 Pro Arg Ile Leu Tyr Asn Pro Leu Gln Gly Gln Lys Cys Ile Val Gln  
 220 225 230  
 aca act tca tgg tcc cag tgc tca aag acc tgt gga act ggt atc tcc 953  
 Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr Gly Ile Ser  
 235 240 245  
 aca cga gtt acc aat gac aac cct gag tgc cgc ctt gtg aaa gaa acc 1001  
 Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys Glu Thr  
 250 255 260  
 cgg att tgt gag gtg cgg cct tgt gga cag cca gtg tac agc agc ctg 1049  
 Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Val Tyr Ser Ser Leu  
 265 270 275 280  
 aaa aag ggc aag aaa tgc agc aag acc aag aaa tcc ccc gaa cca gtc 1097  
 Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys Lys Ser Pro Glu Pro Val  
 285 290 295  
 agg ttt act tac gct gga tgt ttg agt gtg aag aaa tac cgg ccc aag 1145  
 Arg Phe Thr Tyr Ala Gly Cys Leu Ser Val Lys Lys Tyr Arg Pro Lys  
 300 305 310  
 tac tgc ggt tcc tgc gtg gac ggc cga tgc tgc acg ccc cag ctg acc 1193

Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Gln Leu Thr  
 315 320 325  
 agg act gtc aag atg cgg ttc cgc tgc gaa gat ggg gag aca ttt tcc 1241  
 Arg Thr Val Lys Met Arg Phe Arg Cys Glu Asp Gly Glu Thr Phe Ser  
 330 335 340  
 aag aac gtc atg atg atc cag tcc tgc aaa tgc aac tac aac tgc ccg 1289  
 Lys Asn Val Met Met Ile Gln Ser Cys Lys Cys Asn Tyr Asn Cys Pro  
 345 350 355 360  
 cat gcc aat gaa gca gcg ttt ccc ttc tac agg ctg ttc aat gac att 1337  
 His Ala Asn Glu Ala Ala Phe Pro Phe Tyr Arg Leu Phe Asn Asp Ile  
 365 370 375  
 cac aaa ttt agg gac taaatgctac ctgggtttcc agggcacacc tagacaaaca 1392  
 His Lys Phe Arg Asp  
 380  
 agggagaaga gtgtcagaat cagaatcatg gagaaaatgg gcggggglgg tgtgggtgat 1452  
 gggactcatt gtgaaagga agccttgctc attcttgagg agcattaagg tatttcgaaa 1512  
 ctgccaaggg tgctgggtgcg gatggacact aatgcagcca cgattggaga atactttgct 1572  
 tcatagtatt ggagcacatg ttactgcttc attttggagc ttgtggaglt gatgactttc 1632  
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 gtcttacagt cgtaaaagag ataataagat tagttggaca gtttaaagct tttattcgtc 1752  
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 ctgaatgttt tatttatcaa aatgtagctt ttggggaggg aggggaaatg taatactgga 1932  
 ataatttgta aatgatitaa atttatatt cagtgaaaag attttatitaa tggaattaac 1992  
 catitaaataa agaaatattt acct 2016

&lt;211&gt; 381

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu  
1 5 10 15  
His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys  
20 25 30  
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp  
35 40 45  
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys  
50 55 60  
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe  
65 70 75 80  
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu  
85 90 95  
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser  
100 105 110  
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val  
115 120 125  
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly  
130 135 140  
Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu  
145 150 155 160  
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp  
165 170 175

Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu  
 180 185 190  
 Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Ser Ser Leu Lys  
 195 200 205  
 Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu  
 210 215 220  
 Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser  
 225 230 235 240  
 Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro  
 245 250 255  
 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys  
 260 265 270  
 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys  
 275 280 285  
 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu  
 290 295 300  
 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly  
 305 310 315 320  
 Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg  
 325 330 335  
 Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser  
 340 345 350  
 Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro  
 355 360 365  
 Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp  
 370 375 380

&lt;210&gt; 47

&lt;211&gt; 2743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (240).. (2387)

&lt;400&gt; 47

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cgcgcgcgcg tgagcccggg gcgagggctg tcttcccgga gacccgaccc cggcagcgcg 180
ggcgggccac ttctccigig cctccgcccc ctgctccact ccccgccgcc gccgcgcgg 239
atg cca agc acc agc ttt cca gtc cct tcc aag ttt cca ctt ggc cct 287
Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro
      1           5           10           15
gcg gct gcg gtc ttc ggg aga gga gaa act ttg ggg ccc gcg ccg cgc 335
Ala Ala Ala Val Phe Gly Arg Gly Glu Thr Leu Gly Pro Ala Pro Arg
           20           25           30
gcc ggc ggc acc atg aag tca gcg gag gaa gaa cac tat ggc tat gca 383
Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala
           35           40           45
tcc tcc aac gtc agc ccc gcc ctg ccg ctc ccc acg gcg cac tcc acc 431
Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr
           50           55           60
ctg ccg gcc ccg tgc cac aac ctt cag acc tcc aca ccg ggc atc atc 479
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile
           65           70           75           80

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ccg ccg gcg gat cac ccc tcg ggg tac gga gca gct ttg gac ggt ggg 527  
 Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly  
                     85                    90                    95  
 ccc gcg ggc tac ttc ctc tcc tcc ggc cac acc agg cct gat ggg gcc 575  
 Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala  
                     100                    105                    110  
 cct gcc ctg gag agt cct cgc atc gag ata acc tcg tgc ttg ggc ctg 623  
 Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu  
                     115                    120                    125  
 tac cac aac aat aac cag ttt ttc cac gat gtg gag gtg gaa gac gtc 671  
 Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val  
                     130                    135                    140  
 ctc cct agc tcc aaa cgg tcc ccc tcc acg gcc acg ctg agt ctg ccc 719  
 Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro  
 145                    150                    155                    160  
 agc ctg gag gcc tac aga gac ccc tcg tgc ctg agc ccg gcc agc agc 767  
 Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser  
                     165                    170                    175  
 ctg tcc tcc cgg agc tgc aac tca gag gcc tcc tcc tac gag tcc aac 815  
 Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn  
                     180                    185                    190  
 tac tcg tac ccg tac gcg tcc ccc cag acg tcg cca tgg cag tct ccc 863  
 Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro  
                     195                    200                    205  
 tgc gtg tct ccc aag acc acg gac ccc gag gag ggc ttt ccc cgc ggg 911  
 Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly

210	215	220	
ctg ggg gcc tgc aca ctg ctg ggt tcc ccg cag cac tcc ccc tcc acc	959		
Leu Gly Ala Cys Thr Leu Leu Gly Ser Pro Gln His Ser Pro Ser Thr			
225	230	235	240
tcc ccc cgc gcc agc gtc act gag gag agc tgg ctg ggt gcc cgc tcc	1007		
Ser Pro Arg Ala Ser Val Thr Glu Glu Ser Trp Leu Gly Ala Arg Ser			
245	250	255	
tcc aga ccc gcg tcc cct tgc aac aag agg aag tac agc ctc aac ggc	1055		
Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly			
260	265	270	
cgg cag ccg ccc tac tca ccc cac cac tcc ccc acg ccg tcc ccg cac	1103		
Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His			
275	280	285	
ggc tcc ccg cgg gtc agc gtg acc gac gac tcc tgg ttg ggc aac acc	1151		
Gly Ser Pro Arg Val Ser Val Thr Asp Asp Ser Trp Leu Gly Asn Thr			
290	295	300	
acc cag tac acc agc tcc gcc atc gtg gcc gcc atc aac gcg ctg acc	1199		
Thr Gln Tyr Thr Ser Ser Ala Ile Val Ala Ala Ile Asn Ala Leu Thr			
305	310	315	320
acc gac agc agc ctg gac ctg gga gat ggc gtc cct gtc aag tcc cgc	1247		
Thr Asp Ser Ser Leu Asp Leu Gly Asp Gly Val Pro Val Lys Ser Arg			
325	330	335	
aag acc acc ctg gag cag ccg ccc tca gtg gcg ctc aag gtg gag ccc	1295		
Lys Thr Thr Leu Glu Gln Pro Pro Ser Val Ala Leu Lys Val Glu Pro			
340	345	350	
gtc ggg gag gac ctg ggc agc ccc ccg ccc ccg gcc gac ttc gcg ccc	1343		
Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro			

355	360	365	
gaa gac tac tcc tct ttc cag cac atc agg aag ggc ggc ttc tgc gac			1391
Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp			
370	375	380	
cag tac ctg gcg gig ccg cag cac ccc tac cag tgg gcg aag ccc aag			1439
Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys			
385	390	395	400
ccc ctg tcc cct acg tcc tac atg agc ccg acc ctg ccc gcc ctg gac			1487
Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp			
405	410	415	
tgg cag ctg ccg tcc cac tca ggc ccg tat gag ctt cgg att gag gtg			1535
Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val			
420	425	430	
cag ccc aag tcc cac cac cga gcc cac tac gag acg gag ggc agc ccg			1583
Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg			
435	440	445	
ggg gcc gtg aag gcg tcc gcc gga gga cac ccc atc gtg cag ctg cat			1631
Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His			
450	455	460	
ggc tac ttg gag aat gag ccg ctg atg ctg cag ctt ttc att ggg acg			1679
Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr			
465	470	475	480
gcg gac gac cgc ctg ctg cgc ccg cac gcc ttc tac cag gtg cac cgc			1727
Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg			
485	490	495	
atc aca ggg aag acc gtg tcc acc acc agc cac gag gct atc ctc tcc			1775

Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser  
 500 505 510  
 aac acc aaa gtc ctg gag atc cca ctc ctg ccg gag aac agc atg cga 1823  
 Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg  
 515 520 525  
 gcc gtc att gac tgt gcc gga atc ctg aaa ctc aga aac tcc gac att 1871  
 Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile  
 530 535 540  
 gaa ctt cgg aaa gga gag acg gac atc ggg agg aag aac aca cgg gta 1919  
 Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val  
 545 550 555 560  
 cgg ctg gtg ttc cgc gtt cac gtc ccg caa ccc agc ggc cgc acg ctg 1967  
 Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu  
 565 570 575  
 tcc ctg cag gtg gcc tcc aac ccc atc gaa tgc tcc cag cgc tca gct 2015  
 Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala  
 580 585 590  
 cag gag ctg cct ctg gtg gag aag cag agc acg gac agc tat ccg gtc 2063  
 Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val  
 595 600 605  
 gtg ggc ggg aag aag atg gtc ctg tct ggc cac aac ttc ctg cag gac 2111  
 Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp  
 610 615 620  
 tcc aag gtc att ttc gtg gag aaa gcc cca gat ggc cac cat gtc tgg 2159  
 Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp  
 625 630 635 640  
 gag atg gaa gcg aaa act gac cgg gac ctg tgc aag ccg aat tct ctg 2207

Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu  
                     645                    650                    655  
 gtg gtt gag atc ccg cca ttt cgg aat cag agg ata acc agc ccc gtt 2255  
 Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val  
                     660                    665                    670  
 cac gtc agt ttc tac gtc tgc aac ggg aag aga aag cga agc cag tac 2303  
 His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr  
                     675                    680                    685  
 cag cgt ttc acc tac ctt ccc gcc aac ggt aac gcc atc ttt cta acc 2351  
 Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr  
                     690                    695                    700  
 gta agc cgt gaa cat gag cgc gtg ggg tgc ttt ttc taaagacgca 2397  
 Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe  
                     705                    710                    715  
 gaaacgacgt cgccgtaaag cagcgtggcg tgttgcacat tlaacigtgt gatgtcccg 2457  
 tagtgagacc gagccatcga tgcctgaaa aggaaaggaa aagggaagct tcggatgcat 2517  
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 ttttgcttct tgcgaatgta taacagccaa ggggaaaaca tggctcttct gctccaaaaa 2637  
 actgaggggg tcctggtgtg catttgcacc cttaaagctgc ttacggtgaa aaggcaaata 2697  
 ggtatagcta ttttgcaggc accttagga ataaactttg ctttta 2743

&lt;210&gt; 48

&lt;211&gt; 716

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro

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20 25 30  
Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala  
35 40 45  
Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr  
50 55 60  
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile  
65 70 75 80  
Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly  
85 90 95  
Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala  
100 105 110  
Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu  
115 120 125  
Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val  
130 135 140  
Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro  
145 150 155 160  
Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser  
165 170 175  
Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn  
180 185 190  
Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro  
195 200 205  
Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly

210	215	220	
Leu Gly Ala Cys Thr	Leu Leu Gly Ser Pro Gln His	Ser Pro Ser Thr	
225	230	235	240
Ser Pro Arg Ala Ser Val Thr	Glu Glu Ser Trp Leu Gly Ala Arg Ser		
	245	250	255
Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser	Leu Asn Gly		
260	265	270	
Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His			
275	280	285	
Gly Ser Pro Arg Val Ser Val Thr Asp Asp Ser Trp Leu Gly Asn Thr			
290	295	300	
Thr Gln Tyr Thr Ser Ser Ala Ile Val Ala Ala Ile Asn Ala Leu Thr			
305	310	315	320
Thr Asp Ser Ser Leu Asp Leu Gly Asp Gly Val Pro Val Lys Ser Arg			
	325	330	335
Lys Thr Thr Leu Glu Gln Pro Pro Ser Val Ala Leu Lys Val Glu Pro			
340	345	350	
Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro			
355	360	365	
Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp			
370	375	380	
Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys			
385	390	395	400
Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp			
	405	410	415
Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val			
420	425	430	

Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg  
 435 440 445  
 Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His  
 450 455 460  
 Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr  
 465 470 475 480  
 Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg  
 485 490 495  
 Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser  
 500 505 510  
 Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg  
 515 520 525  
 Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile  
 530 535 540  
 Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val  
 545 550 555 560  
 Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu  
 565 570 575  
 Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala  
 580 585 590  
 Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val  
 595 600 605  
 Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp  
 610 615 620  
 Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp  
 625 630 635 640



Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu

645

650

655

Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val

660

665

670

His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr

675

680

685

Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr

690

695

700

Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe

705

710

715

<210> 49

<211> 2353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (241).. (1482)

<400> 49

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ccgcccgcgc gccgccctcc tccctctgcc ttcctccccc acggccggcc gcctcctcgc 180

ccgcccgcgc gcagccgagg agccgaggcc gccgcggccg tggcggcgga gccctcagcc 240

atg gcc tcg ggc gac acc ctc tac atc gcc acg gac ggc tcg gag atg 288

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met

1

5

10

15

ccg gcc gag atc gtg gag ctg cac gag atc gag gtg gag acc atc ccg 336

Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro  
                   20                          25                          30  
 gtg gag acc atc gag acc aca gtg gtg ggc gag gag gag gag gag gac 384  
 Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Glu Asp  
                   35                          40                          45  
 gac gag gag gag gag ggc ggc ggt ggc gag cac ggc ggc ggc ggc ggc 432  
 Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly  
                   50                          55                          60  
 cac ggc cac gcc ggc cac cac cac cac cat cac cac cac cac cac 480  
 His Gly His Ala Gly His His His His His His His His His His His  
                   65                          70                          75                          80  
 ccg ccc atg atc gct ctg cag ccg ctg gtc acc gag gag ccg acc cag 528  
 Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln  
                   85                          90                          95  
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 Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val  
                   100                          105                          110  
 gtg ggc ggc gag gag tcg gag ggc ctg cgc gcc gag gag ggc ttc gag 624  
 Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu  
                   115                          120                          125  
 gat cag att ctc atc ccg gtg ccc gcg ccg gcc ggc ggc gag gag gag 672  
 Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp  
                   130                          135                          140  
 tac att gaa caa acg ctg gtc acc gtg gcg gcg gcc ggc aag agc ggc 720  
 Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly  
                   145                          150                          155                          160  
 ggc ggc ggc tcg tcg tcg tcg gga ggc ggc cgc gtc aag aag ggc ggc 768

Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly  
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 ggc aag aag agc ggc aag aag agt tac ctc agc ggc ggg gcc ggc gcg 816  
 Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala  
                     180                    185                    190  
 gcg ggc ggg cgc ggc gcc gac ccg ggc aac aag aag tgg gag cag aag 864  
 Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys  
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 cag gtg cag atc aag acc ctg gag ggc gag ttc tcg gtc acc atg tgg 912  
 Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp  
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 tcc tca gat gaa aaa aaa gat att gac cat gag aca gtg gtt gaa gaa 960  
 Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu  
                     225                    230                    235                    240  
 cag atc att gga gag aac tca cct cct gat tat tca gaa tat atg aca 1008  
 Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr  
                     245                    250                    255  
 gga aag aaa ctt cct cct gga gga ala cct ggc att gac ctc tca gat 1056  
 Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp  
                     260                    265                    270  
 ccc aaa caa ctg gca gaa ttt gct aga atg aag cca aga aaa att aaa 1104  
 Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys  
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 gaa gat gat gct cca aga aca ata gct tgc cct cat aaa ggc tgc aca 1152  
 Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr  
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Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His  
305 310 315 320  
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Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu  
325 330 335  
agt tca aaa cta aaa cga cac caa ctg gtt cat act gga gag aag ccc 1296  
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro  
340 345 350  
ttt cag tgc acg ttc gaa ggc tgt ggg aaa cgc ttt tca ctg gac ttc 1344  
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe  
355 360 365  
aat ttg cgc aca cat gtg cga atc cat acc gga gac agg ccc tat gtg 1392  
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val  
370 375 380  
tgc ccc ttc gat ggt tgt aat aag aag ttt gct cag tca act aac ctg 1440  
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu  
385 390 395 400  
aaa tct cac atc tta aca cat gct aag gcc aaa aac aac cag 1482  
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln  
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 aaaaaaaaaag ttatataggt ttgttttgct atcttaattt tggttgtatt ctltgatgtt 2082  
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<211> 414

<212> PRT

<213> Homo sapiens

<400> 50

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Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro

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Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Asp

35 40 45

Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly

50 55 60

His Gly His Ala Gly His His His His His His His His His His

65 70 75 80

Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln

85 90 95

Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val  
100 105 110

Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu  
115 120 125

Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp  
130 135 140

Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly  
145 150 155 160

Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly  
165 170 175

Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala  
180 185 190

Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys  
195 200 205

Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp  
210 215 220

Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu  
225 230 235 240

Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr  
245 250 255

Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp  
260 265 270

Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys  
275 280 285

Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr  
290 295 300

Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His  
 305                      310                      315                      320  
 Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu  
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 Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro  
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 Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe  
                          355                      360                      365  
 Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val  
                          370                      375                      380  
 Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu  
 385                      390                      395                      400  
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 ccaacattac ttgagtcctt ggataaaatt gagaaaagag tctacaagta ttgtggactc 180  
 tacaggaggc aggaggctga caactggcag taaagacaaa g atg tca ggc ctg cgg 236

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ccc	ggc	act	caa	gtg	gac	cct	gag	att	gag	ctt	ttt	gta	aag	gct	gga	284
Pro	Gly	Thr	Gln	Val	Asp	Pro	Glu	Ile	Glu	Leu	Phe	Val	Lys	Ala	Gly	
					10		15			20						
agt	gat	gga	gag	agt	att	gga	aac	tgt	ccc	ttt	tgc	caa	cgc	ctt	ttc	332
Ser	Asp	Gly	Glu	Ser	Ile	Gly	Asn	Cys	Pro	Phe	Cys	Gln	Arg	Leu	Phe	
					25		30			35						
atg	atc	ctc	tgg	ctt	aaa	gga	gtt	aaa	ttt	aat	gtg	aca	act	gtt	gac	380
Met	Ile	Leu	Trp	Leu	Lys	Gly	Val	Lys	Phe	Asn	Val	Thr	Thr	Val	Asp	
					40		45			50						
atg	acc	aga	aag	cct	gaa	gaa	cta	aag	gac	tta	gcc	cca	ggt	acc	aat	428
Met	Thr	Arg	Lys	Pro	Glu	Glu	Leu	Lys	Asp	Leu	Ala	Pro	Gly	Thr	Asn	
					55		60			65						
cct	ccg	ttc	ctg	gtg	tat	aac	aag	gag	ttg	aaa	aca	gac	ttc	att	aaa	476
Pro	Pro	Phe	Leu	Val	Tyr	Asn	Lys	Glu	Leu	Lys	Thr	Asp	Phe	Ile	Lys	
					70		75			80			85			
att	gag	gag	ttt	tta	gaa	caa	acc	ctg	gct	cct	cca	agg	tac	cct	cac	524
Ile	Glu	Glu	Phe	Leu	Glu	Gln	Thr	Leu	Ala	Pro	Pro	Arg	Tyr	Pro	His	
					90		95			100						
ctg	agt	ccc	aag	tac	aag	gag	tct	ttt	gat	gtg	ggc	tgt	aac	ctc	ttt	572
Leu	Ser	Pro	Lys	Tyr	Lys	Glu	Ser	Phe	Asp	Val	Gly	Cys	Asn	Leu	Phe	
					105		110			115						
gcc	aag	ttt	tct	gca	tac	att	aag	aat	aca	caa	aag	gag	gca	aat	aag	620
Ala	Lys	Phe	Ser	Ala	Tyr	Ile	Lys	Asn	Thr	Gln	Lys	Glu	Ala	Asn	Lys	
					120		125			130						
aat	ttt	gaa	aaa	tct	ctg	ctc	aaa	gaa	ttc	aag	cgt	ctg	gat	gac	tac	668



Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys Arg Leu Asp Asp Tyr  
 135 140 145  
 tta aac acc cca ctt ctg gat gaa att gat cca gac agt gct ggg gaa 716  
 Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro Asp Ser Ala Gly Glu  
 150 155 160 165  
 ccc cca gtt tcc aga aga cta ttc ttg gat ggg gac cag cta aca ctg 764  
 Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly Asp Gln Leu Thr Leu  
 170 175 180  
 gct gat tgt agc ttg tta ccc aag ctg aac att att aaa gtt gct gcc 812  
 Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile Ile Lys Val Ala Ala  
 185 190 195  
 aag aaa tat cgt gac ttt gac att cca gca gaa ttc tca gga gtc tgg 860  
 Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu Phe Ser Gly Val Trp  
 200 205 210  
 cgt tat ctc cac aat gcc tat gcc cgt gaa gaa ttt acc cac acg tgt 908  
 Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu Phe Thr His Thr Cys  
 215 220 225  
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 Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala Asn Val Ala  
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WO 01/25427

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

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 Cys Gln Arg Leu Phe Met Ile Leu Trp Leu Lys Gly Val Lys Phe Asn  
 35 40 45  
 Val Thr Thr Val Asp Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu  
 50 55 60  
 Ala Pro Gly Thr Asn Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys  
 65 70 75 80  
 Thr Asp Phe Ile Lys Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro  
 85 90 95  
 Pro Arg Tyr Pro His Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val  
 100 105 110  
 Gly Cys Asn Leu Phe Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln  
 115 120 125  
 Lys Glu Ala Asn Lys Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys  
 130 135 140  
 Arg Leu Asp Asp Tyr Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro  
 145 150 155 160  
 Asp Ser Ala Gly Glu Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly  
 165 170 175

Asp Gln Leu Thr Leu Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile

180

185

190

Ile Lys Val Ala Ala Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu

195

200

205

Phe Ser Gly Val Trp Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu

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Phe Thr His Thr Cys Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala

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230

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Asn Val Ala

<210> 53

<211> 4001

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (316)

<400> 53

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5

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15

att gcc aag aag aaa acc cat gtg aag aag tgc act ttg aac ccc atc 97

Ile Ala Lys Lys Lys Thr His Val Lys Lys Cys Thr Leu Asn Pro Ile

20

25

30

ttc aat gaa tct ttc atc tac gac atc ccc act gac ctc ctg cct gat 145

Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp

35

40

45

atc agc atc gag ttc ctc gtt atc gac ttc gat cgc acc acc aag aat 193  
 Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn  
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 gag gtg gtg ggg agg ctg atc ctc ggg gca cac agt gtc aca gcc agt 241  
 Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser  
 65 70 75 80  
 ggt gct gaa cac tgg aga gag gtc tgc gag agc ccc cgc aag cct gtg 289  
 Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val  
 85 90 95  
 gcc aag tgg cac agt ctc agc gag tac taatcctgtt cttctctcct 336  
 Ala Lys Trp His Ser Leu Ser Glu Tyr  
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<210> 54

<211> 105

<212> PRT

<213> Homo sapiens

<400> 54

Pro Gly Asn Pro Tyr Val Lys Val Asn Val Tyr Tyr Gly Arg Lys Arg  
 1 5 10 15  
 Ile Ala Lys Lys Lys Thr His Val Lys Lys Cys Thr Leu Asn Pro Ile  
 20 25 30  
 Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp  
 35 40 45  
 Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn  
 50 55 60  
 Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser  
 65 70 75 80  
 Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val  
 85 90 95  
 Ala Lys Trp His Ser Leu Ser Glu Tyr  
 100 105

<210> 55

<211> 952

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118).. (909)

<400> 55

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 ggcitctgga ggaaagagaa ggagggcagt gctccagtgg tacagaagtg agacata 117  
 atg gaa tca ggc ttc acc tcc aag gac acc tat cia agc cat ttt aac 165  
 Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His Phe Asn

1	5	10	15	
cct cgg gat tac cta gaa aaa tat tac aag ttt ggt tct agg cac tct	213			
Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser				
20	25	30		
gca gaa agc cag att ctt aag cac ctt ctg aaa aat ctt ttc aag ata	261			
Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile				
35	40	45		
ttc tgc cta gac ggt gtg aag gga gac ctg ctg att gac atc ggc tct	309			
Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser				
50	55	60		
ggc ccc act atc tat cag ctc ctc tct gct tgt gaa tcc ttt aag gag	357			
Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu				
65	70	75	80	
atc gtc gtc act gac tac tca gac cag aac ctg cag gag ctg gag aag	405			
Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys				
85	90	95		
tgg ctg aag aaa gag cca gag gcc ttt gac tgg tcc cca gtg gtg acc	453			
Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr				
100	105	110		
tat gtg tgt gat ctt gaa ggg aac aga gtc aag ggt cca gag aag gag	501			
Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu				
115	120	125		
gag aag ttg aga cag gcg gtc aag cag gtg ctg aag tgt gat gtg act	549			
Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr				
130	135	140		
cag agc cag cca ctg ggg gcc gtc ccc tta ccc ccg gct gac tgc gtg	597			
Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val				



145	150	155	160	
ctc agc aca ctg tgt ctg gat gcc gcc tgc cca gac ctc ccc acc tac				645
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr				
	165	170	175	
tgc agg gcg ctc agg aac ctc ggc agc cta ctg aag cca ggg ggc ttc				693
Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe				
	180	185	190	
ctg gtg atc atg gat gcg ctc aag agc agc tac tac atg att ggt gag				741
Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu				
	195	200	205	
cag aag ttc tcc agc ctc ccc ctg ggc cgg gag gca gta gag gct gct				789
Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala				
	210	215	220	
gtg aaa gag gct ggc tac aca atc gaa tgg ttt gag gtg atc tcg caa				837
Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln				
	225	230	235	240
agt tat tct tcc acc atg gcc aac aac gaa gga ctt ttc tcc ctg gtg				885
Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val				
	245	250	255	
gcg agg aag ctg agc aga ccc ctg tgatgcctgt gacctcaatt aaagcaattc				939
Ala Arg Lys Leu Ser Arg Pro Leu				
	260			
ctttgacctg tca				952

&lt;210&gt; 56

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His Phe Asn  
1 5 10 15  
Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser  
20 25 30  
Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile  
35 40 45  
Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser  
50 55 60  
Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu  
65 70 75 80  
Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys  
85 90 95  
Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr  
100 105 110  
Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu  
115 120 125  
Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr  
130 135 140  
Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val  
145 150 155 160  
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr  
165 170 175  
Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe  
180 185 190

Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu

195

200

205

Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala

210

215

220

Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln

225

230

235

240

Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val

245

250

255

Ala Arg Lys Leu Ser Arg Pro Leu

260

<210> 57

<211> 2617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94).. (633)

<400> 57

tagaggatcc aagcctacgt acgcgtccgg agaccgcttg tgctggagtc ggagttgtaa 60

cgcctccactg actgatagag cgaccggccg acc atg gcg ccc gga gtg gcc cgc 114

Met Ala Pro Gly Val Ala Arg

1

5

ggg ccg acg ccg tac tgg agg ttg cgc ctc ggt ggc gcc gcg ctg ctc 162

Gly Pro Thr Pro Tyr Trp Arg Leu Arg Leu Gly Gly Ala Ala Leu Leu

10

15

20

ctg ctg ctc atc ccg gtg gcc gcc gcg cag gag cct ccc gga gct gct 210

Leu Leu Leu Ile Pro Val Ala Ala Ala Gln Glu Pro Pro Gly Ala Ala  
 25 30 35  
 tgt tct cag aac aca aac aaa acc tgt gaa gag tgc ctg aag aac gtc 258  
 Cys Ser Gln Asn Thr Asn Lys Thr Cys Glu Glu Cys Leu Lys Asn Val  
 40 45 50 55  
 tcc tgt ctt tgg tgc aac act aac aag gct tgt ctg gac tac cca gtt 306  
 Ser Cys Leu Trp Cys Asn Thr Asn Lys Ala Cys Leu Asp Tyr Pro Val  
 60 65 70  
 aca agc gtc ttg cca ccg gct tcc ctt tgt aaa ttg agc tct gca cgc 354  
 Thr Ser Val Leu Pro Pro Ala Ser Leu Cys Lys Leu Ser Ser Ala Arg  
 75 80 85  
 tgg gga gtt tgt tgg gtg aac ttt gag gcg ctg atc atc acc atg tgc 402  
 Trp Gly Val Cys Trp Val Asn Phe Glu Ala Leu Ile Ile Thr Met Ser  
 90 95 100  
 gta gtc ggg gga acc ctc ctc ctg ggc att gcc atc tgc tgc tgc tgc 450  
 Val Val Gly Gly Thr Leu Leu Leu Gly Ile Ala Ile Cys Cys Cys Cys  
 105 110 115  
 tgc tgc agg agg aag agg agc cgg aag ccg gac agg agt gag gag aag 498  
 Cys Cys Arg Arg Lys Arg Ser Arg Lys Pro Asp Arg Ser Glu Glu Lys  
 120 125 130 135  
 gcc atg cgt gag cgg gag gag agg cgg ata cgg cag gag gaa cgg aga 546  
 Ala Met Arg Glu Arg Glu Glu Arg Arg Ile Arg Gln Glu Glu Arg Arg  
 140 145 150  
 gca gag atg aag aca aga cat gat gaa atc aga aaa aaa tat ggc ctg 594  
 Ala Glu Met Lys Thr Arg His Asp Glu Ile Arg Lys Lys Tyr Gly Leu  
 155 160 165  
 ttt aaa gaa gaa aac ccg tat gct aga ttt gaa aac aac taaagcgctc 643

Phe Lys Glu Glu Asn Pro Tyr Ala Arg Phe Glu Asn Asn

170

175

180

cagcacatca gtcccgacgc ttcctgtgag gtgcacaccg cagcccagcc cagccgggag 703  
accacgtggc cattgcggtc tcttgacctt ggccagtga cctgccagcc ticcaggaca 763  
ggcggccgga gagctgcccc tgaaggacag tctctctgtc ttgcagacig gtgaccttct 823  
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taacaagctt cacacgaac acagggaagt cggtttgact ttgttcatga ggagaactga 1063  
ccagccctca tcattcccca taaaaccacg gacagcgtct gtgtgcgcat ctgagctctt 1123  
cacacctgtt gactcacacg gcttttgctg atgacacggg gctccagtac acagctgat 1183  
aaggacttaa cgtcctaacc tcaattgtat taaatagcat tggggaatag ctaaaccttt 1243  
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gtaagcagac caagcgcttc gtggcaggga aagcagcgtg cggggaagtc actgaaaagt 1903  
gctgcclaag gaagtttgga aatagtcacc gtccagatt gccttgaatt taaaacatt 1963  
ttgccttggg aaagtaggtc agcagcacct aagatcaagg atgcgttcca ttctcacact 2023  
tcacagtcac gaaaactgag aagactgtct tcagcgtgaa ctaaagtcca caggcagatc 2083

actgatccag aacacttcaa gaactcgcca aacagctcga taagccitit tgactgtgta 2143  
 catctgtacc gggaataaca ttcttaggct gaaatttcca caaagaatag aacctgtacc 2203  
 cagtcttcca ggctgatttc cctgacctct tgggcatttg tattttagt aaagtattgc 2263  
 agagattcct aaglatitita tagcagccat caaaattgga ctttgtattg ttatlcata 2323  
 aaagacactt ggtaatagac ttcagtgaac tctgtatgaa tgcagtagtg tgtgtgcaaa 2383  
 atccgcttcc tgagcgtagg gtgctgagct ggcgctagg ctcggttggt aaatacagcg 2443  
 tagtcagccc ttgcgctcag tgtagaaacc cacgtctgta aggtcggctc tcgtccatct 2503  
 gcttttttct gaaatacact aagagcagcc aaaaactgt aacctcaagg aaaccataaa 2563  
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<210> 58

<211> 180

<212> PRT

<213> Homo sapiens

<400> 58

Met Ala Pro Gly Val Ala Arg Gly Pro Thr Pro Tyr Trp Arg Leu Arg

1 5 10 15

Leu Gly Gly Ala Ala Leu Leu Leu Leu Ile Pro Val Ala Ala Ala

20 25 30

Gln Glu Pro Pro Gly Ala Ala Cys Ser Gln Asn Thr Asn Lys Thr Cys

35 40 45

Glu Glu Cys Leu Lys Asn Val Ser Cys Leu Trp Cys Asn Thr Asn Lys

50 55 60

Ala Cys Leu Asp Tyr Pro Val Thr Ser Val Leu Pro Pro Ala Ser Leu

65 70 75 80

Cys Lys Leu Ser Ser Ala Arg Trp Gly Val Cys Trp Val Asn Phe Glu

85 90 95

Ala Leu Ile Ile Thr Met Ser Val Val Gly Gly Thr Leu Leu Leu Gly

100

105

110

Ile Ala Ile Cys Cys Cys Cys Cys Cys Arg Arg Lys Arg Ser Arg Lys

115

120

125

Pro Asp Arg Ser Glu Glu Lys Ala Met Arg Glu Arg Glu Glu Arg Arg

130

135

140

Ile Arg Gln Glu Glu Arg Arg Ala Glu Met Lys Thr Arg His Asp Glu

145

150

155

160

Ile Arg Lys Lys Tyr Gly Leu Phe Lys Glu Glu Asn Pro Tyr Ala Arg

165

170

175

Phe Glu Asn Asn

180

<210> 59

<211> 3217

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (469).. (1875)

<400> 59

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ctccctgttt ccttccigt ccttcccagc tcacgtctc ttctccigcc gccigccttt 180  
cttttttct ttttttgcatt ggcgctcttg gggctgttac acacacgcgc gctgtccatt 240  
gcagcttaca taaaggcggg cgcgattatg caattatatt gtttagcgata ttcaagagc 300  
aatggctcgt tttcttagga ttcaacacg aaggcatcat gcatttttga aaaactagta 360

ttgagaataa taccttgcaa cgtaaagaat gtttttgggt atttttacac aatcictact 420

ttgaccaaac gagtcggac agttttcttt laattgaaaa taggagaa atg gag gaa 477

Met Glu Glu

1

aga atg gaa atg att tct gaa agg cca aaa gag agt atg tat tcc tgg 525

Arg Met Glu Met Ile Ser Glu Arg Pro Lys Glu Ser Met Tyr Ser Trp

5

10

15

aac aaa act gca gag aaa agt gat ttt gaa gct gta gaa gca ctt atg 573

Asn Lys Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu Ala Leu Met

20

25

30

35

tca atg agc tgc agt tgg aag tct gat ttt aag aaa tac gtt gaa aac 621

Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr Val Glu Asn

40

45

50

aga cct gtt aca cca gta tct gat ttg tca gag gaa gag aat ctg ctt 669

Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu Asn Leu Leu

55

60

65

ccg gga aca cct gat ttt cat aca atc cca gca ttt tgt itg act cca 717

Pro Gly Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys Leu Thr Pro

70

75

80

cct tac agt cct tct gac ttt gaa ccc tct caa gtg tca aat ctg atg 765

Pro Tyr Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser Asn Leu Met

85

90

95

gca cca gcg cca tct act gta cac ttc aag tca ctc tca gat act gcc 813

Ala Pro Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser Asp Thr Ala

100

105

110

115

aaa cct cac att gcc gca cct ttc aaa gag gaa gaa aag agc cca gta 861

Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys Ser Pro Val



120	125	130	
tct gcc ccc aaa ctc ccc aaa gct cag gca aca agt gtg att cgt cat	909		
Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His			
135	140	145	
aca gct gat gcc cag cta tgt aac cac cag acc tgc cca atg aaa gca	957		
Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro Met Lys Ala			
150	155	160	
gcc agc atc ctc aac tat cag aac aat tct ttt aga aga aga acc cac	1005		
Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg Arg Thr His			
165	170	175	
cta aat gtt gag gct gca aga aag aac ata cca tgt gcc gct gtg tca	1053		
Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala Ala Val Ser			
180	185	190	195
cca aac aga tcc aaa tgt gag aga aac aca gtg gca gat gtt gat gag	1101		
Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp Val Asp Glu			
200	205	210	
aaa gca agt gct gca ctt tat gac ttt tct gtg cct tcc tca gag acg	1149		
Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser Ser Glu Thr			
215	220	225	
gtc atc tgc agg tct cag cca gcc cct gtg tcc cca caa cag aag tca	1197		
Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln Gln Lys Ser			
230	235	240	
gtg ttg gtc tct cca cct gca gta tct gca ggg gga gtg cca cct atg	1245		
Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val Pro Pro Met			
245	250	255	
ccg gtc atc tgc cag atg gtt ccc ctt cct gcc aac aac cct gtt gtg	1293		

Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn Pro Val Val  
 260 265 270 275  
 aca aca gtc gtt ccc agc act cct ccc agc cag cca cca gct gtt tgc 1341  
 Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys  
 280 285 290  
 ccc cct gtt gtg ttc atg ggc aca caa gtc ccc aaa ggc gct gtc atg 1389  
 Pro Pro Val Val Phe Met Gly Thr Gln Val Pro Lys Gly Ala Val Met  
 295 300 305  
 ttt gtg gta ccc cag ccc gtt gtg cag agt tca aag cct ccg gtg gtg 1437  
 Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro Pro Val Val  
 310 315 320  
 agc ccg aat ggc acc aga ctc tct ccc att gcc cct gct cct ggg ttt 1485  
 Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe  
 325 330 335  
 tcc cct tca gca gca aaa gtc act cct cag att gat tca tca agg ata 1533  
 Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser Ser Arg Ile  
 340 345 350 355  
 agg agt cac atc tgt agc cac cca gga tgt ggc aag aca tac ttt aaa 1581  
 Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys  
 360 365 370  
 agt tcc cat ctg aag gcc cac acg agg acg cac aca gga gaa aag cct 1629  
 Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly Glu Lys Pro  
 375 380 385  
 ttc agc tgt agc tgg aaa ggt tgt gaa agg agg ttt gcc cgt tct gat 1677  
 Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp  
 390 395 400  
 gaa ctg tcc aga cac agg cga acc cac acg ggt gag aag aaa ttt gcg 1725

Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala  
 405 410 415  
 tgc ccc atg tgt gac cgg cgg ttc atg agg agt gac cat ttg acc aag 1773  
 Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys  
 420 425 430 435  
 cat gcc cgg cgc cat cta tca gcc aag aag cta cca aac tgg cag atg 1821  
 His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met  
 440 445 450  
 gaa gtg agc aag cta aat gac att gct cta cct cca acc cct gct ccc 1869  
 Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Pro  
 455 460 465  
 aca cag tgacagaccg gaaagtgaag agtcagaact aactttggtc tcagcgggag 1925  
 Thr Gln  
 ccagtggatga tgtaaaaatg cttccactgc aagtcctgtgg cccacaacg tggcttaaag 1985  
 cagaagcccc acagcctggc acgaaggccc cgtctgggtt aggtgactaa aagggtctcg 2045  
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 tgattaaata tatctagaac tatcatTTTT acactattgt gaatatTTGG aattgaacga 2465  
 ctgtatatgt ctaagagggc caaagaattg gaatcctcct taatttaatt gctttgaagc 2525  
 atagctacaa ttgtttttg catttttgtt ttgaaagttt aacaaatgac tgtaictagg 2585  
 catttcattg tgccttgaac tttagtttgc ctgcagtttc ttgtgtagat ttgaaaattg 2645  
 tataccaacg tgtttctgt agactctaag atacactgca ctttgtttag aaaaaaaact 2705

gaagatgaaa tatatatgt aaagaaggga tattaagaat ctiagataac ticttgaaaa 2765  
 agatggccta tgtcalcagc aaaglacctc catgitatga ggalataatg tgtgcctcat 2825  
 tgaattagaa aattagtgac cattattcac aggtggacaa atgtgtcct gtaatttat 2885  
 aggagttttt tgggatgtgg aggiagtgg gtagaaaaat tatiagaaca ttcacitttg 2945  
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 aagtacattg cttaaaatat atagigaaaa atgtcactat atcttcccat ttaacattgt 3065  
 ttttgtatat tgggtgtaga tttctgacat caaaacttgg acccttggaa aacaaaagtt 3125  
 ttaattaaaa aaaatccttg tgacttaciaa ttgcacaat atttctttg tigtacttta 3185  
 tatcttgttt acaataaaga attccctttg gc 3217

<210> 60

<211> 469

<212> PRT

<213> Homo sapiens

<400> 60

Met Glu Glu Arg Met Glu Met Ile Ser Glu Arg Pro Lys Glu Ser Met

1 5 10 15

Tyr Ser Trp Asn Lys Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu

20 25 30

Ala Leu Met Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr

35 40 45

Val Glu Asn Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu

50 55 60

Asn Leu Leu Pro Gly Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys

65 70 75 80

Leu Thr Pro Pro Tyr Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser

85 90 95

Asn Leu Met Ala Pro Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser  
100 105 110  
Asp Thr Ala Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys  
115 120 125  
Ser Pro Val Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val  
130 135 140  
Ile Arg His Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro  
145 150 155 160  
Met Lys Ala Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg  
165 170 175  
Arg Thr His Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala  
180 185 190  
Ala Val Ser Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp  
195 200 205  
Val Asp Glu Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser  
210 215 220  
Ser Glu Thr Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln  
225 230 235 240  
Gln Lys Ser Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val  
245 250 255  
Pro Pro Met Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn  
260 265 270  
Pro Val Val Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro  
275 280 285  
Ala Val Cys Pro Pro Val Val Phe Met Gly Thr Gln Val Pro Lys Gly  
290 295 300  
Ala Val Met Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro

305                      310                      315                      320  
Pro Val Val Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala  
                         325                      330                      335  
Pro Gly Phe Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser  
                         340                      345                      350  
Ser Arg Ile Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr  
                         355                      360                      365  
Tyr Phe Lys Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly  
                         370                      375                      380  
Glu Lys Pro Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala  
385                      390                      395                      400  
Arg Ser Asp Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys  
                         405                      410                      415  
Lys Phe Ala Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His  
                         420                      425                      430  
Leu Thr Lys His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn  
                         435                      440                      445  
Trp Gln Met Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr  
                         450                      455                      460  
Pro Ala Pro Thr Gln  
465

&lt;210&gt; 61

&lt;211&gt; 1428

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (125).. (868)

&lt;400&gt; 61

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cgagctgata aaggcgccat ttggagggg ccgcgggaga cgtggcgccg ctgcgggcctc 60
gcctcgccgt gcgctaggct tgggggaag gccigtctc gagtcgcgc ttctgcac 120
cgcc atg tgc gga ggt ggt gtg att cgt ggc ccc gca ggg aac aac gat 169
      Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp
          1             5             10             15
tgc cgc atc tac gtg ggt aac tta cct cca gac atc cga acc aag gac 217
Cys Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp
          20             25             30
att gag gac gtg ttc tac aaa tac ggc gct atc cgc gac atc gac ctc 265
Ile Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu
          35             40             45
aag aat cgc cgc ggg gga ccg ccc ttc gcc ttc gtt gag ttc gag gac 313
Lys Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp
          50             55             60
ccg cga gac gcg gaa gac gcg gtg tat ggt cgc gac ggc tat gat tac 361
Pro Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr
          65             70             75
gat ggg tac cgt ctg cgg gtg gag ttt cct cga agc ggc cgt gga aca 409
Asp Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr
          80             85             90             95
ggc cga ggc ggc ggc ggg ggt gga ggt ggc gga gct ccc cga ggt cgc 457
Gly Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg
          100             105             110

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tat ggc ccc cca tcc agg cgg tct gaa aac aga gtg gtt gtc tct gga 505  
 Tyr Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly  
 115 120 125  
 ctg cct cca agt gga agt tgg cag gat tta aag gat cac atg cgt gaa 553  
 Leu Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu  
 130 135 140  
 gca ggt gat gla tgt tat gct gat gtt tac cga gat ggc act ggt gtc 601  
 Ala Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val  
 145 150 155  
 gtg gag ttt gla cgg aaa gaa gat atg acc tat gca gtt cga aaa ctg 649  
 Val Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu  
 160 165 170 175  
 gat aac act aag ttt aga tct cat gag gga gaa act gcc tac atc cgg 697  
 Asp Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg  
 180 185 190  
 gtt aaa gtt gat ggg ccc aga agt cca agt tat gga aga tct cga tct 745  
 Val Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser  
 195 200 205  
 cga agc cgt agt cgt agc aga agc cgt agc aga agc aac agc agg agt 793  
 Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser  
 210 215 220  
 cgc agt tac tcc cca agg aga agc aga gga tca cca cgc tat tct ccc 841  
 Arg Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro  
 225 230 235  
 cgt cat agc aga tct cgc tct cgt aca taagatgatt ggtgacactt 888  
 Arg His Ser Arg Ser Arg Ser Arg Thr  
 240 245



ttgtagaac ccaatgtgta tacagttttc ctttattcag tacaatcttt tcatttttta 948  
 attcaaactg ttgtgttcag aatgggctaa agtgttgaal tgcattcttg taatacccc 1008  
 ttgctcctaa catctacatt cccctcgtgi ctttgataaa ttgtatttta agtgaatgca 1068  
 tagacaggat tgtttaaatt tagttaactc catactcttc agactgtgat attgtgtaaa 1128  
 tgtctatcig cccgtgtttg tgtgaactgg gatgttgggg gtgtttgtgg ttatcttacc 1188  
 tggggaagtt cttatgttta tcttgctttt catgtgtctt tctgtagaca tatctgaaga 1248  
 gatggattaa gaatgctttg gattaaaggat tgtggagcac atttcaatca ttttaggatt 1308  
 gtcaaaagga ggattgagga ggaacagatc aataatggag gcaatgggat gactccaagt 1368  
 gctattgtca cagaatgaaat tggcagtatt gacctatcac taaaaggcag gggctaaaaa 1428

<210> 62

<211> 248

<212> PRT

<213> Homo sapiens

<400> 62

Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp Cys

1 5 10 15

Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp Ile

20 25 30

Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu Lys

35 40 45

Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp Pro

50 55 60

Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr Asp

65 70 75 80

Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr Gly

85 90 95

Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg Tyr

100

105

110

Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly Leu

115

120

125

Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu Ala

130

135

140

Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val Val

145

150

155

160

Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu Asp

165

170

175

Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg Val

180

185

190

Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser Arg

195

200

205

Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser Arg

210

215

220

Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro Arg

225

230

235

240

His Ser Arg Ser Arg Ser Arg Thr

245

&lt;210&gt; 63

&lt;211&gt; 3664

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (195).. (1943)

&lt;400&gt; 63

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 ccccaggact tctgtgactc ctgggccaca gaggiccaac cagggttaagg gcctggggat 120  
 accccctgcc tggccccctt gcccaaactg gcaggggggc caggctgggc agcagccccct 180  
 ctitcacctc aact atg gat ctc ctg ccc ccc aag ccc aag tac aat cca 230

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro

1 5 10

ctc cgg aat gag tct ctg tca tcg ctg gag gaa ggg gct tct ggg tcc 278  
 Leu Arg Asn Glu Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser

15 20 25

acc ccc ccg gag gag ctg cct tcc cca tca gct tca tcc ctg ggg ccc 326  
 Thr Pro Pro Glu Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro

30 35 40

atc ctg cct cct ctg cct ggg gac gat agt ccc act acc ctg tgc tcc 374  
 Ile Leu Pro Pro Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser

45 50 55 60

ttc ttc ccc cgg atg agc aac ctg agg ctg gcc aac ccg gct ggg ggg 422  
 Phe Phe Pro Arg Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly

65 70 75

cgc cca ggg tct aag ggg gag cca gga agg gca gct gat gat ggg gag 470  
 Arg Pro Gly Ser Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu

80 85 90

ggg atc gat ggg gca gcc atg cca gag tca ggc ccc cta ccc ctc ctc 518  
 Gly Ile Asp Gly Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu

95 100 105

cag gac atg aac aag ctg agt gga ggc ggc ggg cgc agg act cgg gtg 566  
 Gln Asp Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val  
 110 115 120  
 gaa ggg ggc cag ctt ggg ggc gag gag tgg acc cgc cac ggg agc ttt 614  
 Glu Gly Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe  
 125 130 135 140  
 gtc aat aag ccc acg cgg ggc tgg ctg cat ccc aac gac aaa gtc atg 662  
 Val Asn Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met  
 145 150 155  
 gga ccc ggg gtt tcc tac ttg gtt cgg tac atg ggt tgt gtg gag gtc 710  
 Gly Pro Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val  
 160 165 170  
 ctc cag tca atg cgt gcc ctg gac ttc aac acc cgg act cag gtc acc 758  
 Leu Gln Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr  
 175 180 185  
 agg gag gcc atc agt ctg gtg tgt gag gct gtg ccg ggt gct aag ggg 806  
 Arg Glu Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly  
 190 195 200  
 gcg aca agg agg aga aag ccc tgt agc cgc ccg ctc agc tct atc ctg 854  
 Ala Thr Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu  
 205 210 215 220  
 ggg agg agt aac ctg aaa ttt gct gga atg cca atc act ctc acc gtc 902  
 Gly Arg Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val  
 225 230 235  
 tcc acc agc agc ctc aac ctc atg gcc gca gac tgc aaa cag atc atc 950  
 Ser Thr Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile  
 240 245 250

gcc aac cac cac atg caa tct atc tca ttt gca tcc ggc ggg gat ccg 998  
 Ala Asn His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro  
 255 260 265  
 gac aca gcc gag tat gtc gcc tat gtt gcc aaa gac cct gtg aat cag 1046  
 Asp Thr Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln  
 270 275 280  
 aga gcc tgc cac att ctg gag tgt ccc gaa ggg ctt gcc cag gat gtc 1094  
 Arg Ala Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val  
 285 290 295 300  
 atc agc acc att ggc cag gcc ttc gag ttg cgc ttc aaa caa tac ctc 1142  
 Ile Ser Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu  
 305 310 315  
 agg aac cca ccc aaa ctg gtc acc cct cat gac agg atg gct ggc ttt 1190  
 Arg Asn Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe  
 320 325 330  
 gat ggc tca gca tgg gat gag gag gag gaa gag cca cct gac cat cag 1238  
 Asp Gly Ser Ala Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln  
 335 340 345  
 tac tat aat gac ttc ccg ggg aag gaa ccc ccc ttg ggg ggg gtg gta 1286  
 Tyr Tyr Asn Asp Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val  
 350 355 360  
 gac atg agg ctt cgg gaa gga gcc gct cca ggg gct gct cga ccc act 1334  
 Asp Met Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr  
 365 370 375 380  
 gca ccc aat gcc cag acc ccc agc cac ttg gga gct aca ttg cct gta 1382  
 Ala Pro Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val

385	390	395	
gga cag cct gtt ggg gga gat cca gaa gtc cgc aaa cag atg cca cct	1430		
Gly Gln Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro			
400	405	410	
cca cca ccc tgt cca ggc aga gag ctt ttt gat gat ccc tcc tat gtc	1478		
Pro Pro Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val			
415	420	425	
aac gtc cag aac cta gac aag gcc cgg caa gca gtg ggt ggt gct ggg	1526		
Asn Val Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly			
430	435	440	
ccc ccc aat cct gct atc aat ggc agt gca ccc cgg gac ctg ttt gac	1574		
Pro Pro Asn Pro Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp			
445	450	455	460
atg aag ccc ttc gaa gat gct ctt cgg gtg cct cca cct ccc cag tgc	1622		
Met Lys Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser			
465	470	475	
gtg tcc atg gct gag cag ctc cga ggg gag ccc tgg ttc cat ggg aag	1670		
Val Ser Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys			
480	485	490	
ctg agc cgg cgg gag gct gag gca ctg ctg cag ctc aat ggg gac ttc	1718		
Leu Ser Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe			
495	500	505	
tig gta cgg gag agc acg acc aca cct ggc cag tat gtg ctc act ggc	1766		
Leu Val Arg Glu Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly			
510	515	520	
tig cag agt ggg cag cct aag cat ttg cta ctg gtg gac cct gag ggt	1814		
Leu Gln Ser Gly Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly			

525                      530                      535                      540  
 gtg gtt cgg act aag gat cac cgc ttt gaa agt gtc agt cac ctt atc 1862  
 Val Val Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile  
                          545                      550                      555  
 agc tac cac atg gac aat cac ttg ccc atc atc tct gcg ggc agc gaa 1910  
 Ser Tyr His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu  
                          560                      565                      570  
 ctg tgt cta cag caa cct gtg gag cgg aaa ctg tgatctgccc tagcgtcttc 1963  
 Leu Cys Leu Gln Gln Pro Val Glu Arg Lys Leu  
                          575                      580  
 ttccagaaga tgccctccaa tcccttccac cctattccct aactctcggg acctcgtttg 2023  
 ggagtgttct gtgggcttgg ccttgtgtca gagctgggag tagcatggac tctgggtttc 2083  
 atatccagct gagtgagagg gtttgagtca aaagcctggg tgagaatcct gccctcctcc 2143  
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 ccaaccgat gcccttctcc caagaagggt agtgcttgic atggaaaatg tctgtgtgtg 2263  
 acaggcccag tggaacagtc accttcttgg gcaaggggga acaaatcaca cctctgggct 2323  
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 aatgacaggg atgccaacac ctcttgggt tctgggacct gtgtcttgc tgagcacct 2503  
 ctccggtttg ggttgggata acagaggcag gattggcagc tgtccctct ccttggggat 2563  
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 ccttgcctca gtgccctctg gccggggccc ctaccccaa ggggtcigta tataatttc 2683  
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 tctgaagcc tctgccctgc ctcccttct gggagggcgg ggtgggggtg actgaatttg 2803  
 ggcctcttgt acagttaact ctcccagggt gattttgtgg aggtgagaaa aggggcattg 2863  
 agactataaa gcagtagaca atccccacat accatctgta gatttggaa tgcatcttt 2923

taaagtttta taigcalata ttttagggct gctagactta ctttcctatt ttcttttcca 2983  
 ttgcttatic ttgagcacia aatgataalc aattattaca ttataacalc acctttttga 3043  
 cttttccaag cccitttaca gctcttggca ttttcctcgc ctaggccgtg gagtlaactg 3103  
 ggatcgcacc tttatacca gagacctgag gcagatgaaa ttattttcca tctaggacta 3163  
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 ataagggaga gttgaccgtt ttcattctgg cctccctttg ctgtttggat gtttccacgg 3403  
 gtctcactta taccaaaggg aaaactcttc attaaagtcg gtatttcttc taaaaaaaaa 3463  
 aaaaaaaaaa tacatttata catcaccttt ttgacttttc caagcccttt tacagctctt 3523  
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<210> 64

<211> 583

<212> PRT

<213> Homo sapiens

<400> 64

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro Leu Arg Asn Glu

1 5 10 15

Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser Thr Pro Pro Glu

20 25 30

Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro

35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg

50 55 60



WO 01/25427

Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly Arg Pro Gly Ser  
 65 70 75 80  
 Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu Gly Ile Asp Gly  
 85 90 95  
 Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu Gln Asp Met Asn  
 100 105 110  
 Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln  
 115 120 125  
 Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro  
 130 135 140  
 Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val  
 145 150 155 160  
 Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met  
 165 170 175  
 Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile  
 180 185 190  
 Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg  
 195 200 205  
 Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg Ser Asn  
 210 215 220  
 Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr Ser Ser  
 225 230 235 240  
 Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn His His  
 245 250 255  
 Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr Ala Glu  
 260 265 270  
 Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala Cys His

275	280	285	
Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile			
290	295	300	
Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro			
305	310	315	320
Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala			
325	330	335	
Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp			
340	345	350	
Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu			
355	360	365	
Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro Asn Ala			
370	375	380	
Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln Pro Val			
385	390	395	400
Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro Pro Cys			
405	410	415	
Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val Gln Asn			
420	425	430	
Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro Asn Pro			
435	440	445	
Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe			
450	455	460	
Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser Met Ala			
465	470	475	480
Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg			

485 490 495  
 Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu  
 500 505 510  
 Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly  
 515 520 525  
 Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr  
 530 535 540  
 Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met  
 545 550 555 560  
 Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln  
 565 570 575  
 Gln Pro Val Glu Arg Lys Leu  
 580

<210> 65

<211> 2493

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (41).. (1237)

<400> 65

actgcgactc gagacagcgg ccgggcagga cagctccaga atg aaa atg cgg ttc 55

Met Lys Met Arg Phe

1 5

ttg ggg ttg gtg gtc tgt ttg gtt ctc tgg ccc ctg cat tct gag ggg 103

Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro Leu His Ser Glu Gly

10	15	20	
tct gga ggg aaa ctg aca gct gtg gat cct gaa aca aac atg aat gtg			151
Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu Thr Asn Met Asn Val			
25	30	35	
agt gaa att atc tct tac tgg gga ttc cct agt gag gaa tac cta gtt			199
Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser Glu Glu Tyr Leu Val			
40	45	50	
gag aca gaa gat gga tat att ctg tgc ctt aac cga att cct cat ggg			247
Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn Arg Ile Pro His Gly			
55	60	65	
agg aag aac cat tct gac aaa ggt ccc aaa cca gtt gtc ttc ctg caa			295
Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro Val Val Phe Leu Gln			
70	75	80	85
cat ggc ttg ctg gca gat tct agt aac tgg gtc aca aac ctt gcc aac			343
His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val Thr Asn Leu Ala Asn			
90	95	100	
agc agc ctg ggc ttc att ctt gct gat gct ggt ttt gac gtg tgg atg			391
Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp Val Trp Met			
105	110	115	
ggc aac agc aga gga aat acc tgg tct cgg aaa cat aag aca ctc tca			439
Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Lys Thr Leu Ser			
120	125	130	
gtt tct cag gat gaa ttc tgg gct ttc agt tat gat gag atg gca aaa			487
Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu Met Ala Lys			
135	140	145	
tat gac cta cca gct tcc att aac ttc att ctg aat aaa act ggc caa			535
Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu Asn Lys Thr Gly Gln			

150	155	160	165	
gaa caa gtg tat tat gtg ggt cat tct caa ggc acc act ala ggt ttt				583
Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly Thr Thr Ile Gly Phe				
	170	175	180	
ata gca ttt tca cag atc cct gag ctg gct aaa agg att aaa atg ttt				631
Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys Arg Ile Lys Met Phe				
	185	190	195	
ttt gcc ctg ggt cct gtg gct tcc gtc gcc ttc tgt act agc cct atg				679
Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe Cys Thr Ser Pro Met				
	200	205	210	
gcc aaa tta gga cga tta cca gat cat ctc att aag gac tta ttt gga				727
Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile Lys Asp Leu Phe Gly				
	215	220	225	
gac aaa gaa ttt ctt ccc cag agt gcg ttt ttg aag tgg ctg ggt acc				775
Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu Lys Trp Leu Gly Thr				
	230	235	240	245
cac gtt tgc act cat gtc ata ctg aag gag ctc tgt gga aat ctc tgt				823
His Val Cys Thr His Val Ile Leu Lys Glu Leu Cys Gly Asn Leu Cys				
	250	255	260	
ttt ctt ctg tgt gga ttt aat gag aga aat tta aat atg tct aga gtg				871
Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu Asn Met Ser Arg Val				
	265	270	275	
gat gta tat aca aca cat tct cct gct gga act tct gtg caa aac atg				919
Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr Ser Val Gln Asn Met				
	280	285	290	
tta cac tgg agc cag gct gtt aaa ttc caa aag ttt caa gcc ttt gac				967

Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys Phe Gln Ala Phe Asp  
 295 300 305  
 tgg gga agc agt gcc aag aat tat ttt cat tac aac cag agt tat cct 1015  
 Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr Asn Gln Ser Tyr Pro  
 310 315 320 325  
 ccc aca tac aat gtg aag gac atg ctt gtg ccg act gca gtc tgg agc 1063  
 Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro Thr Ala Val Trp Ser  
 330 335 340  
 ggg ggt cac gac tgg ctt gca gat gtc tac gac gtc aat atc tta ctg 1111  
 Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp Val Asn Ile Leu Leu  
 345 350 355  
 act cag atc acc aac ttg gtg ttc cat gag agc att ccg gaa tgg gag 1159  
 Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser Ile Pro Glu Trp Glu  
 360 365 370  
 cat ctt gac ttc att tgg ggc ctg gat gcc cct tgg agg ctt tat aat 1207  
 His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro Trp Arg Leu Tyr Asn  
 375 380 385  
 aaa att att aat cta atg agg aaa tat cag tgaaagctgg acttgagctg 1257  
 Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln  
 390 395  
 tgtaccacca agtcaatgat tatgtcatgt gaaaatgtgt ttgcttcatt tctgtaaaac 1317  
 acttgttttt ctttcccagg tcttttgttt ttttatatcc aagaaaatga taactttgaa 1377  
 gatgccagct tcactctagt ttcaattaga aacatactag ctattttttc ttttaattagg 1437  
 gctggaatag gaagccagtg tcicaacat agtatgtct ctttaagtct tttaaatc 1497  
 actgaigtgt aaaaaggica ttatatccat tctgttttta aaatttaaaa tatattgact 1557  
 ttttgccctt cataggacaa agtaatatat ggttggaat tttaaaattg tgttgctcatt 1617  
 ggtaaactctg tcactgactt aagcgaggta taaaagiact cagttttcat gtccttgcc 1677

taaagagctc tctagctcaa cggctcttgta gttagagatc taaatgacat ttatcatgt 1737  
 tttccctgcag caggctgcata gtcaaatcca gaaatatcac agctgtgccca glaataagga 1797  
 tgctaacaat taattttatc aaacctaaact gtgacagcig tgatttgaca cgttttaatt 1857  
 gctcaggtaa aatgaaatag ttttccggcg tcttcaaaaa caaattgcac tgataaaaca 1917  
 aaaacaaaag tatgttttaa atgctttgaa gactgataca ctcaaccatc tataatcatg 1977  
 agctctcaat ttcatggcag gccatagttc tacitattcg agaagcaaat cccctiggag 2037  
 actalaccac tattttttct gagattaatg tactcttggg gcccgctact gtcgttattg 2097  
 atcacatcig tctgaagcca aagccccgtg gtigcccatg agaagtgtcc ttgttcattt 2157  
 tcacccaaat gaagtgtgaa cgtgatgttt tcggatgcaa actcagctca gggattcatt 2217  
 ttgtgtctta gttttataig catccttatt ttttaatacac ctgcttcacg tccctatgtt 2277  
 gggaagtcga tatttgcctg cttttcttgc agcatcattt ccttacaata ctgtccggtg 2337  
 gacaaaatga caattgatat gttttcttga tataattact ttagctgcac taacagtaca 2397  
 atgcttgtaa atggttaata taggcagggc gaatactact ttgttaacttt taaagcttta 2457  
 aacttttcaa taaaattgag tgagacttat aggcc 2493

<210> 66

<211> 399

<212> PRT

<213> Homo sapiens

<400> 66

Met Lys Met Arg Phe Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro

1

5

10

15

Leu His Ser Glu Gly Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu

20

25

30

Thr Asn Met Asn Val Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser

35

40

45

Glu Glu Tyr Leu Val Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn

50	55	60	
Arg Ile Pro His Gly Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro			
65	70	75	80
Val Val Phe Leu Gln His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val			
85	90	95	
Thr Asn Leu Ala Asn Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly			
100	105	110	
Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys			
115	120	125	
His Lys Thr Leu Ser Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr			
130	135	140	
Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu			
145	150	155	160
Asn Lys Thr Gly Gln Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly			
165	170	175	
Thr Thr Ile Gly Phe Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys			
180	185	190	
Arg Ile Lys Met Phe Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe			
195	200	205	
Cys Thr Ser Pro Met Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile			
210	215	220	
Lys Asp Leu Phe Gly Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu			
225	230	235	240
Lys Trp Leu Gly Thr His Val Cys Thr His Val Ile Leu Lys Glu Leu			
245	250	255	
Cys Gly Asn Leu Cys Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu			



260 265 270  
Asn Met Ser Arg Val Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr  
275 280 285  
Ser Val Gln Asn Met Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys  
290 295 300  
Phe Gln Ala Phe Asp Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr  
305 310 315 320  
Asn Gln Ser Tyr Pro Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro  
325 330 335  
Thr Ala Val Trp Ser Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp  
340 345 350  
Val Asn Ile Leu Leu Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser  
355 360 365  
Ile Pro Glu Trp Glu His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro  
370 375 380  
Trp Arg Leu Tyr Asn Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln  
385 390 395

<210> 67

<211> 1633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (323).. (1177)

<400> 67

aacttaatgt ttttgcatg gactttgagt taagattatt ttttaaacc tgaggactag 60

cattaatga cagctgaccc aggtgctaca cagaagtgga ttcagtgaat cttaggaagac 120  
 agcagcagac aggatccag gaaccaggtt ttgatgaagc taggactgag gagcaagcga 180  
 gcaagcagca gttcgtggaa tctgtctgc tgctgtcttc ctggtttagg agccgacggg 240  
 cgctcgcagg ctccagcgcg gctgcccgcg gcaggacccg gccgcctccg ccgccgccgc 300  
 cgcccctaag cctcccgaag cc atg gcc ggg ctc ggc cac ccc gcc gcc ttc 352

Met Ala Gly Leu Gly His Pro Ala Ala Phe

1 5 10

ggc cgg gcc acc cac gcc gtg gtg cgg gcg cta ccc gag tcg ctc ggc 400  
 Gly Arg Ala Thr His Ala Val Val Arg Ala Leu Pro Glu Ser Leu Gly

15 20 25

cag cac gcg ctg aga agc gcc aag ggc gag gag gtg gac gtc gcc cgc 448  
 Gln His Ala Leu Arg Ser Ala Lys Gly Glu Glu Val Asp Val Ala Arg

30 35 40

gcg gaa cgg cag cac cag ctc tac gtg ggc glg ctg ggc agc aag ctg 496  
 Ala Glu Arg Gln His Gln Leu Tyr Val Gly Val Leu Gly Ser Lys Leu

45 50 55

ggg ctg cag gtg gtg gag ctg ccg gcc gac gag agc ctt ccg gac tgc 544  
 Gly Leu Gln Val Val Glu Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys

60 65 70

gtc ttc gtg gag gac gtg gcc glg gtg tgc gag gag acg gcc ctc atc 592  
 Val Phe Val Glu Asp Val Ala Val Val Cys Glu Glu Thr Ala Leu Ile

75 80 85 90

acc cga ccc ggg gcg ccg agc cgg agg aag gag gtt gac atg atg aaa 640  
 Thr Arg Pro Gly Ala Pro Ser Arg Arg Lys Glu Val Asp Met Met Lys

95 100 105

gaa gca tta gaa aaa ctt cag ctc aat ata gta gag atg aaa gat gaa 688  
 Glu Ala Leu Glu Lys Leu Gln Leu Asn Ile Val Glu Met Lys Asp Glu

110	115	120	
aat gca act tta gat ggc gga gat gtt tta ttc aca ggc aga gaa ttt	736		
Asn Ala Thr Leu Asp Gly Gly Asp Val Leu Phe Thr Gly Arg Glu Phe			
125	130	135	
ttt gtg ggc ctt tcc aaa agg aca aat caa cga ggt gct gaa atc ttg	784		
Phe Val Gly Leu Ser Lys Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu			
140	145	150	
gct gat act ttt aag gac tat gca gtc tcc aca gtg cca gtg gca gat	832		
Ala Asp Thr Phe Lys Asp Tyr Ala Val Ser Thr Val Pro Val Ala Asp			
155	160	165	170
ggg ttg cat ttg aag agt ttc tgc agc atg gct ggg cct aac ctg atc	880		
Gly Leu His Leu Lys Ser Phe Cys Ser Met Ala Gly Pro Asn Leu Ile			
175	180	185	
gca att ggg tct agt gaa tct gca cag aag gcc ctt aag atc atg caa	928		
Ala Ile Gly Ser Ser Glu Ser Ala Gln Lys Ala Leu Lys Ile Met Gln			
190	195	200	
cag atg agt gac cac cgc tac gac aaa ctc act gtg cct gat gac ata	976		
Gln Met Ser Asp His Arg Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile			
205	210	215	
gca gca aac tgt ata tat cta aat atc ccc aac aaa ggg cac gtc ttg	1024		
Ala Ala Asn Cys Ile Tyr Leu Asn Ile Pro Asn Lys Gly His Val Leu			
220	225	230	
ctg cac cga acc ccg gaa gag tat cca gaa agt gca aag gtt tat gag	1072		
Leu His Arg Thr Pro Glu Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu			
235	240	245	250
aaa ctg aag gac cat atg ctg atc ccc gtg agc atg tct gaa ctg gaa	1120		

Lys Leu Lys Asp His Met Leu Ile Pro Val Ser Met Ser Glu Leu Glu

255 260 265

aag gtg gat ggg ctg ctc acc tgc tgc tca gtt tta att aac aag aaa 1168

Lys Val Asp Gly Leu Leu Thr Cys Cys Ser Val Leu Ile Asn Lys Lys

270 275 280

gta gac tcc tgagctgcag agtccccccc ggtagccggc aagaccgcac 1217

Val Asp Ser

285

aggcaaggcc gatgactctg tgcccactcc tgttgttttc cttgacaatc tactgtgccca 1277

ctgtgctact aactcttggt tacaaaaattt gattctaagt tgaattgctt cattcaacac 1337

ccccaccctc cctccccreg aggtgggtacc taagctgtgg atttgctaaa tgaattaagc 1397

aacctagaag atacagagct aatgaattat caaaatgiga ttaatcccag taaggaaaca 1457

ctcatttagt gtctgtattt ttgggtgtnaa aattatttag ttgccagtat attctgaaga 1517

atgtcttctt gatcagtcag ataagcttgc tttttttttt tttttttcat gaatcatgtt 1577

tggttctctg gaaagtcctt ggtccaggga tctctctctt tctcttttta cttctg 1633

<210> 68

<211> 285

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Gly Leu Gly His Pro Ala Ala Phe Gly Arg Ala Thr His Ala

1 5 10 15

Val Val Arg Ala Leu Pro Glu Ser Leu Gly Gln His Ala Leu Arg Ser

20 25 30

Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln

35 40 45

Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu

50

55

60

Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val

65

70

75

80

Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro

85

90

95

Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu

100

105

110

Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly

115

120

125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys

130

135

140

Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp

145

150

155

160

Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser

165

170

175

Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu

180

185

190

Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg

195

200

205

Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr

210

215

220

Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu

225

230

235

240

Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met

245

250

255

Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu

260 265 270  
 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser

275 280 285

<210> 69

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147).. (1421)

<400> 69

aagcgctgt ctgaacctct gccagtcctg gagactggcg ccctgagctc caaccagcgg 60  
 gcctcatcta caccctcacc accgcaactt ctaccccgag caagaagcag ctcccagaga 120  
 gaaagaacgt tcccacctgc ctagcc atg gga gag gac gct gca cag gcc gaa 173

Met Gly Glu Asp Ala Ala Gln Ala Glu

1 5

aag ttc cag cac cct ggg tct gac atg cgg cag gaa aag ccc tcg agc 221

Lys Phe Gln His Pro Gly Ser Asp Met Arg Gln Glu Lys Pro Ser Ser

10 15 20 25

ccc agc cgg atg cct tcc tcc aca cca agc ccc agc ctg aac cta ggg 269

Pro Ser Pro Met Pro Ser Ser Thr Pro Ser Pro Ser Leu Asn Leu Gly

30 35 40

aac aca gag gag gcc atc cgg gac aac tca cag gtg aac gca gtc acg 317

Asn Thr Glu Glu Ala Ile Arg Asp Asn Ser Gln Val Asn Ala Val Thr

45 50 55

gtg ctc acg ctc ctg gac aag ctg gtg aac atg cta gac gct gtg cag 365

Val Leu Thr Leu Leu Asp Lys Leu Val Asn Met Leu Asp Ala Val Gln  
 60 65 70  
 gag aac cag cac aag atg gag cag cga cag atc agt ttg gag ggc tcc 413  
 Glu Asn Gln His Lys Met Glu Gln Arg Gln Ile Ser Leu Glu Gly Ser  
 75 80 85  
 gtg aag ggc atc cag aat gac ctc acc aag ctc tcc aag tac cag gcc 461  
 Val Lys Gly Ile Gln Asn Asp Leu Thr Lys Leu Ser Lys Tyr Gln Ala  
 90 95 100 105  
 tcc acc agc aac acg gtg agc aag ctg ctg gag aag tcc cgc aag gtc 509  
 Ser Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys Ser Arg Lys Val  
 110 115 120  
 agc gcc cac acg cgc gcg gtc aaa gag cgc atg gat agg cag tgc gca 557  
 Ser Ala His Thr Arg Ala Val Lys Glu Arg Met Asp Arg Gln Cys Ala  
 125 130 135  
 cag gtg aag cgg ctg gag aac aac cac gcc cag ctc ctc cga cgc aac 605  
 Gln Val Lys Arg Leu Glu Asn Asn His Ala Gln Leu Leu Arg Arg Asn  
 140 145 150  
 cat ttc aaa gtg ctc atc ttc cag gag gaa aat gag atc cct gcc agc 653  
 His Phe Lys Val Leu Ile Phe Gln Glu Glu Asn Glu Ile Pro Ala Ser  
 155 160 165  
 gtg ttt gtg aaa cag ccc gtt tcc ggt gcc gtg gaa ggg aag gag gag 701  
 Val Phe Val Lys Gln Pro Val Ser Gly Ala Val Glu Gly Lys Glu Glu  
 170 175 180 185  
 ctt ccg gat gaa aac aaa tcc ctg gag gaa acc ctg cac acc gtg gac 749  
 Leu Pro Asp Glu Asn Lys Ser Leu Glu Glu Thr Leu His Thr Val Asp  
 190 195 200

ctc tcc tca gat gat gat ttg ccc cac gat gag gag gcc ctg gaa gac 797  
 Leu Ser Ser Asp Asp Asp Leu Pro His Asp Glu Glu Ala Leu Glu Asp  
 205 210 215  
 agt gcc gag gaa aag gtg gaa gaa agt agg gca gag aaa ata aaa aga 845  
 Ser Ala Glu Glu Lys Val Glu Glu Ser Arg Ala Glu Lys Ile Lys Arg  
 220 225 230  
 tcc agc ctg aag aaa gtg gat agc ctc aag aaa gca ttt tct cgc cag 893  
 Ser Ser Leu Lys Lys Val Asp Ser Leu Lys Lys Ala Phe Ser Arg Gln  
 235 240 245  
 aac atc gag aaa aag atg aac aag ctg ggg aca aag atc gta tct gta 941  
 Asn Ile Glu Lys Lys Met Asn Lys Leu Gly Thr Lys Ile Val Ser Val  
 250 255 260 265  
 gag agg aga gag aag att aag aaa tct ctc acg tca aat cac cag aaa 989  
 Glu Arg Arg Glu Lys Ile Lys Lys Ser Leu Thr Ser Asn His Gln Lys  
 270 275 280  
 ata tcc tca gga aaa agc tcc ccc ttc aag gtt tct ccc ctc act ttc 1037  
 Ile Ser Ser Gly Lys Ser Ser Pro Phe Lys Val Ser Pro Leu Thr Phe  
 285 290 295  
 ggg cgg aag aaa gtc cga gag gga gaa agc cat gca gaa aat gag acc 1085  
 Gly Arg Lys Lys Val Arg Glu Gly Glu Ser His Ala Glu Asn Glu Thr  
 300 305 310  
 aag tca gaa gac ctg cct agc agt gag cag atg cca aat gac cag gaa 1133  
 Lys Ser Glu Asp Leu Pro Ser Ser Glu Gln Met Pro Asn Asp Gln Glu  
 315 320 325  
 gag gag tcc ttt gca gag ggt cat tcc gaa gcg tcc ctc gcc agc gct 1181  
 Glu Glu Ser Phe Ala Glu Gly His Ser Glu Ala Ser Leu Ala Ser Ala  
 330 335 340 345



ctg gig gaa ggg gaa att gca gag gag gct gct gag aag gcg acc tcc 1229  
 Leu Val Glu Gly Glu Ile Ala Glu Glu Ala Ala Glu Lys Ala Thr Ser

350

355

360

agg ggg agt aac tcg ggg atg gac agc aac atc gac ttg act att gtg 1277  
 Arg Gly Ser Asn Ser Gly Met Asp Ser Asn Ile Asp Leu Thr Ile Val

365

370

375

gaa gat gaa gag gag gag tca gtg gcc ctg gaa cag gca cag aag gta 1325  
 Glu Asp Glu Glu Glu Glu Ser Val Ala Leu Glu Gln Ala Gln Lys Val

380

385

390

cgc tat gag ggt agc tac gcg cta aca tcc gag gag gcg gag cgc tcc 1373  
 Arg Tyr Glu Gly Ser Tyr Ala Leu Thr Ser Glu Glu Ala Glu Arg Ser

395

400

405

gat ggg gac ccc gtg cag ccc gcc gtg ctc cag gtg cac cag acc tcc 1421  
 Asp Gly Asp Pro Val Gln Pro Ala Val Leu Gln Val His Gln Thr Ser

410

415

420

425

tgagcttaga gccaccgtgc catcctgtgc tgtgtcctcaag cgggcagcca gggctgaaga 1481  
 acaaactcctt gcacatctcc agcacgactc acccactcctt gcgttcctgt ccaggcagta 1541  
 atcattgacc atatagtcac agtaagacac acgagaccag gctttaccat gaaagcgacc 1601  
 tgtcacggac tccactttta atttgccttt aggttctatc tctgtagaat gtctccaaga 1661  
 ttgaagaaga aactgagcag ttgaaaaatg ctaatctctt tgacttagtc agaaaaaac 1721  
 agaggataat taagatacta gtcatgaaaa gtgattcatt cttttttgtc attccatc 1779

&lt;210&gt; 70

&lt;211&gt; 425

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

Met Gly Glu Asp Ala Ala Gln Ala Glu Lys Phe Gln His Pro Gly Ser  
 1 5 10 15  
 Asp Met Arg Gln Glu Lys Pro Ser Ser Pro Ser Pro Met Pro Ser Ser  
 20 25 30  
 Thr Pro Ser Pro Ser Leu Asn Leu Gly Asn Thr Glu Glu Ala Ile Arg  
 35 40 45  
 Asp Asn Ser Gln Val Asn Ala Val Thr Val Leu Thr Leu Leu Asp Lys  
 50 55 60  
 Leu Val Asn Met Leu Asp Ala Val Gln Glu Asn Gln His Lys Met Glu  
 65 70 75 80  
 Gln Arg Gln Ile Ser Leu Glu Gly Ser Val Lys Gly Ile Gln Asn Asp  
 85 90 95  
 Leu Thr Lys Leu Ser Lys Tyr Gln Ala Ser Thr Ser Asn Thr Val Ser  
 100 105 110  
 Lys Leu Leu Glu Lys Ser Arg Lys Val Ser Ala His Thr Arg Ala Val  
 115 120 125  
 Lys Glu Arg Met Asp Arg Gln Cys Ala Gln Val Lys Arg Leu Glu Asn  
 130 135 140  
 Asn His Ala Gln Leu Leu Arg Arg Asn His Phe Lys Val Leu Ile Phe  
 145 150 155 160  
 Gln Glu Glu Asn Glu Ile Pro Ala Ser Val Phe Val Lys Gln Pro Val  
 165 170 175  
 Ser Gly Ala Val Glu Gly Lys Glu Glu Leu Pro Asp Glu Asn Lys Ser  
 180 185 190  
 Leu Glu Glu Thr Leu His Thr Val Asp Leu Ser Ser Asp Asp Asp Leu  
 195 200 205

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Pro His Asp Glu Glu Ala Leu Glu Asp Ser Ala Glu Glu Lys Val Glu  
 210 215 220  
 Glu Ser Arg Ala Glu Lys Ile Lys Arg Ser Ser Leu Lys Lys Val Asp  
 225 230 235 240  
 Ser Leu Lys Lys Ala Phe Ser Arg Gln Asn Ile Glu Lys Lys Met Asn  
 245 250 255  
 Lys Leu Gly Thr Lys Ile Val Ser Val Glu Arg Arg Glu Lys Ile Lys  
 260 265 270  
 Lys Ser Leu Thr Ser Asn His Gln Lys Ile Ser Ser Gly Lys Ser Ser  
 275 280 285  
 Pro Phe Lys Val Ser Pro Leu Thr Phe Gly Arg Lys Lys Val Arg Glu  
 290 295 300  
 Gly Glu Ser His Ala Glu Asn Glu Thr Lys Ser Glu Asp Leu Pro Ser  
 305 310 315 320  
 Ser Glu Gln Met Pro Asn Asp Gln Glu Glu Glu Ser Phe Ala Glu Gly  
 325 330 335  
 His Ser Glu Ala Ser Leu Ala Ser Ala Leu Val Glu Gly Glu Ile Ala  
 340 345 350  
 Glu Glu Ala Ala Glu Lys Ala Thr Ser Arg Gly Ser Asn Ser Gly Met  
 355 360 365  
 Asp Ser Asn Ile Asp Leu Thr Ile Val Glu Asp Glu Glu Glu Glu Ser  
 370 375 380  
 Val Ala Leu Glu Gln Ala Gln Lys Val Arg Tyr Glu Gly Ser Tyr Ala  
 385 390 395 400  
 Leu Thr Ser Glu Glu Ala Glu Arg Ser Asp Gly Asp Pro Val Gln Pro  
 405 410 415  
 Ala Val Leu Gln Val His Gln Thr Ser

420

425

&lt;210&gt; 71

&lt;211&gt; 2638

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (288).. (1844)

&lt;400&gt; 71

gaggaaaggg gaaatgcggc ccgctcccca ctcagtgcc ctcgtgcc ctcctgcc 60  
 ggccctgagg gcacccggtt gctgcttct tccgtcttc cccaaggact atcagagatg 120  
 ccagcgtgac cctgacacg tgtgtgcagc agcctgcagc tgcctcaagc catggctgaa 180  
 cactgactcc cagctgtggg cttcaccatt acagactccc cagggttca aagacttctc 240  
 agcttcgagc atggcttttg gctgtcaggg cagctgtaca atagtgg atg ttt gag 296

Met Phe Glu

1

acg gag gca gat gag aag agg gag atg gcc ttg gag gaa ggg aag ggg 344  
 Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu Gly Lys Gly

5

10

15

cct ggt gcc gag gat tcc cca ccc agc aag gag ccc tct cct ggc cag 392  
 Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser Pro Gly Gln

20

25

30

35

gag ctt cct cca gga caa gac ctt cca ccc aac aag gac tcc cct tct 440  
 Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp Ser Pro Ser

40

45

50

ggg cag gaa ccc gct ccc agc caa gaa cca ctg tcc agc aaa gac tca 488

Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser Lys Asp Ser  
                   55                  60                  65  
 gct acc tct gaa gga tcc cct cca ggc cca gat gct ccg ccc agc aag 536  
 Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro Pro Ser Lys  
                   70                  75                  80  
 gat gtc cca cca tgc cag gaa ccc cct cca gcc caa gac ctc tca ccc 584  
 Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp Leu Ser Pro  
                   85                  90                  95  
 tgc cag gac cta cct gct ggt caa gaa ccc ctg cct cac cag gac cct 632  
 Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His Gln Asp Pro  
 100                  105                  110                  115  
 cta ctc acc aaa gac ctc cct gcc atc cag gaa tcc ccc acc cgg gac 680  
 Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro Thr Arg Asp  
                   120                  125                  130  
 ctt cca ccc tgt caa gat ctg cct cct agc cag gtc tcc ctg cca gcc 728  
 Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser Leu Pro Ala  
                   135                  140                  145  
 aag gcc ctt act gag gac acc atg agc tcc ggg gac cta cta gca gct 776  
 Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu Leu Ala Ala  
                   150                  155                  160  
 act ggg gac cca cct gcg gcc ccc agg cca gcc ttc gtg atc cct gag 824  
 Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val Ile Pro Glu  
                   165                  170                  175  
 gtc cgg ctg gat agc acc tac agc cag aag gca ggg gca gag cag ggc 872  
 Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala Glu Gln Gly  
 180                  185                  190                  195

tgc tgc gga gat gag gag gat gca gaa gag gcc gag gag gtc gag gag 920  
 Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu Val Glu Glu  
 200 205 210  
 ggg gag gaa ggg gag gag gac gag gat gag gac acc agc gat gac aac 968  
 Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser Asp Asp Asn  
 215 220 225  
 tac gga gag cgc agt gag gcc aag cgc agc agc atg atc gag acg ggc 1016  
 Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile Glu Thr Gly  
 230 235 240  
 cag ggg gct gag ggt ggc ctc tca ctg cgt gtc cag aac tcg ctg cgg 1064  
 Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn Ser Leu Arg  
 245 250 255  
 cgc cgg acg cac agc gag ggc agc ctg ctg cag gag ccc cga ggg ccc 1112  
 Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro Arg Gly Pro  
 260 265 270 275  
 tgc ttt gcc tcc gac acc acc ttg cac tgc tca gac ggt gag ggc gcc 1160  
 Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly Glu Gly Ala  
 280 285 290  
 gcc tcc acc tgg ggc atg cct tcg ccc agc acc ctc aag aaa gag ctg 1208  
 Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys Lys Glu Leu  
 295 300 305  
 ggc cgc aat ggt ggc tcc atg cac cac ctt tcc ctc ttc ttc aca gga 1256  
 Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe Phe Thr Gly  
 310 315 320  
 cac agg aag atg agc ggg gct gac acc gtt ggg gat gat gac gaa gcc 1304  
 His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp Asp Glu Ala  
 325 330 335

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tcc cgg aag aga aag agc aaa aac cta gcc aag gac atg aag aac aag 1352
Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met Lys Asn Lys
340          345          350          355
ctg ggg atc ttc aga cgg cgg aat gag tcc cct gga gcc cct ccc gcg 1400
Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala Pro Pro Ala
          360          365          370
ggc aag gca gac aaa atg atg aag tca ttc aag ccc acc tca gag gaa 1448
Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr Ser Glu Glu
          375          380          385
gcc ctc aag tgg ggc gag tcc ttg gag aag ctg ctg gtt cac aaa tac 1496
Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val His Lys Tyr
          390          395          400
ggg tta gca gtg ttc caa gcc ttc ctt cgc act gag ttc agt gag gag 1544
Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe Ser Glu Glu
          405          410          415
aat ctg gag ttc tgg ttg gct tgt gag gac ttc aag aag gtc aag tca 1592
Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys Val Lys Ser
420          425          430          435
cag tcc aag atg gca tcc aag gcc aag aag atc ttt gct gaa tac atc 1640
Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala Glu Tyr Ile
          440          445          450
gcg atc cag gca tgc aag gag gtc aac ctg gac tcc tac acg cgg gag 1688
Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr Thr Arg Glu
          455          460          465
cac acc aag gac aac ctg cag agc gtc acg cgg ggc tgc ttc gac ctg 1736
His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys Phe Asp Leu

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470                      475                      480  
 gca cag aag cgc atc ttc ggg ctc atg gaa aag gac tgc tac cct cgc 1784  
 Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser Tyr Pro Arg  
 485                      490                      495  
 ttt ctc cgt tct gac ctc tac ctg gac ctt att aac cag aag aag atg 1832  
 Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln Lys Lys Met  
 500                      505                      510                      515  
 agt ccc ccg ctt taggggccac tggagtcgag ctacgcgttc acaccaggcg 1884  
 Ser Pro Pro Leu  
 ggctgggtcc cctgccacc tgcctccctg cccctgtga cggagggggc aagcaagccc 1944  
 ccagaggccg tgtctctgga cagacggala gacatacga agcgaggcct ggaccaagag 2004  
 agggccaggc tactggagga gtagaaggat gggccccgtg gggccccac tggcccggtg 2064  
 cgagggggcc caagaccctg gcaggtcagg ggccctggcc aagccagatc tggagctgct 2124  
 gctccctgct gcggagaccg cggaggcttc gcgttgacca agttccttaa agaactggct 2184  
 gatggggcag gaggtccagg cctgggctct cgggccctcc tagaggggca ttggagcttg 2244  
 cagctcagac cccacttg agttttatit atttaaata tagltggatg cttggcacgt 2304  
 cgctctglaa taggaaaccc ttgcctcacc agttttccctg atttacaagt gcaatatit 2364  
 agccaatgcc tigggagaag ctgccatgca aaggtggaca ccattctcca gcttcagggg 2424  
 ataigtctgt cccgggcacc ggtggcaggc agctggcctt ctggactaag gcagcctggg 2484  
 gggacactgc agtctggcga cacacagaga tctggcacc cctgggtgga gtgtccctcg 2544  
 ggggcttttg gaaagcatgg caccctcaga ccacacagta gccaaagtct ggagcaaata 2604  
 aaaggccctgt gttatttctt gttcttgaaa aaaa 2638

&lt;210&gt; 72

&lt;211&gt; 519

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens



WO 01/25427

&lt;400&gt; 72

Met Phe Glu Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu  
 1 5 10 15  
 Gly Lys Gly Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser  
 20 25 30  
 Pro Gly Gln Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp  
 35 40 45  
 Ser Pro Ser Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser  
 50 55 60  
 Lys Asp Ser Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro  
 65 70 75 80  
 Pro Ser Lys Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp  
 85 90 95  
 Leu Ser Pro Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His  
 100 105 110  
 Gln Asp Pro Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro  
 115 120 125  
 Thr Arg Asp Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser  
 130 135 140  
 Leu Pro Ala Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu  
 145 150 155 160  
 Leu Ala Ala Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val  
 165 170 175  
 Ile Pro Glu Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala  
 180 185 190  
 Glu Gln Gly Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu  
 195 200 205

WO 01/25427

Val Glu Glu Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser  
 210 215 220  
 Asp Asp Asn Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile  
 225 230 235 240  
 Glu Thr Gly Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn  
 245 250 255  
 Ser Leu Arg Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro  
 260 265 270  
 Arg Gly Pro Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly  
 275 280 285  
 Glu Gly Ala Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys  
 290 295 300  
 Lys Glu Leu Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe  
 305 310 315 320  
 Phe Thr Gly His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp  
 325 330 335  
 Asp Glu Ala Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met  
 340 345 350  
 Lys Asn Lys Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala  
 355 360 365  
 Pro Pro Ala Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr  
 370 375 380  
 Ser Glu Glu Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val  
 385 390 395 400  
 His Lys Tyr Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe  
 405 410 415

Ser Glu Glu Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys

420

425

430

Val Lys Ser Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala

435

440

445

Glu Tyr Ile Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr

450

455

460

Thr Arg Glu His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys

465

470

475

480

Phe Asp Leu Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser

485

490

495

Tyr Pro Arg Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln

500

505

510

Lys Lys Met Ser Pro Pro Leu

515

&lt;210&gt; 73

&lt;211&gt; 1901

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (250).. (1206)

&lt;400&gt; 73

aaaaaacagc agggttagct tgcctcctcc ctccctcttc agcttccag acactgattc 60  
tggaatgaaa attcaccctgc ctctgagttg gctcctaattg ggggtgggag tgttacttcg 120  
gttcccaggt tggaagatta tctcaccggg ccccagctat ataagctgac cgggtgtggag 180  
gggcccagca gggccaactc cagggtattcc ttccagaca gaaaaacata caagactcct 240

tcagccaac atg atg gia ctg aaa gia gag gaa ctg gtc act gga aag aag 291

Met Met Val Leu Lys Val Glu Glu Leu Val Thr Gly Lys Lys

1

5

10

aat ggc aat ggg gag gca ggg gaa ttc ctt cct gag gat ttc aga gat 339

Asn Gly Asn Gly Glu Ala Gly Glu Phe Leu Pro Glu Asp Phe Arg Asp

15

20

25

30

gga gag tat gaa gct gct gtt act tta gag aag cag gag gat ctg aag 387

Gly Glu Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys

35

40

45

aca ctt cta gcc cac cct gtg acc ctg ggg gag caa cag tgg aaa agc 435

Thr Leu Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser

50

55

60

gag aaa caa cga gag gca gag ctc cca aag aaa aaa cta gaa caa aga 483

Glu Lys Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg

65

70

75

tcc aag ctt gaa aat tta gaa gac ctt gaa ata atc att caa ctg aag 531

Ser Lys Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys

80

85

90

aaa agg aaa aaa tac agg aaa act aaa gtt cca gtt gta aag gaa cca 579

Lys Arg Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro

95

100

105

110

gaa cct gaa atc att acg gaa cct gtg gat gtg cct acg ttt ctg aag 627

Glu Pro Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys

115

120

125

gct gct ctg gag aat aaa ctg cca gta gta gaa aaa ttc ttg tca gac 675

Ala Ala Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp

130

135

140

aag aac aat cca gat gtt tgt gat gag tat aaa cgg aca gct ctt cat 723  
Lys Asn Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His  
145 150 155  
aga gca tgc ttg gaa gga cat ttg gca att gtg gag aag tta atg gaa 771  
Arg Ala Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu  
160 165 170  
gct gga gcc cag atc gaa ttc cgt gat atg ctt gaa tcc aca gcc atc 819  
Ala Gly Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile  
175 180 185 190  
cac tgg gca agc cgt gga gga aac ctg gat gtt tta aaa ttg ttg ctg 867  
His Trp Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu  
195 200 205  
aat aaa gga gca aaa att agc gcc cga gat aag ttg ctc agc aca gcg 915  
Asn Lys Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala  
210 215 220  
ctg cat gtg gcg gtg agg act ggc cac tat gag tgc gcg gag cat ctt 963  
Leu His Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu  
225 230 235  
atc gcc tgt gag gca gac ctc aac gcc aaa gac aga gaa gga gat acc 1011  
Ile Ala Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr  
240 245 250  
ccg ttg cat gat gcg gtg aga ctg aac cgc tat aag atg atc cga ctc 1059  
Pro Leu His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu  
255 260 265 270  
ctg att atg tat ggc gcg gat ctc aac atc aag aac tgt gct ggg aag 1107  
Leu Ile Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys

275 280 285  
 acg ccg atg gat ctg gtg cta cac tgg cag aat gga acc aaa gca ata 1155  
 Thr Pro Met Asp Leu Val Leu His Trp Gln Asn Gly Thr Lys Ala Ile  
 290 295 300  
 ttc gac agc ctc aga gag aac tcc tac aag acc tct cgc ata gct aca 1203  
 Phe Asp Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr  
 305 310 315  
 ttc tgaggcaaac gacagactct taatcagtaa atgttcactg gcattttgaa 1256  
 Phe  
 ggcatggccc aggagaagag acactagcca taaaatctag tttctattta tcaacgtgtt 1316  
 gigaagatgt acctaatgaa gttttgagaa agcacagggt tataggigt taaatttcct 1376  
 ttagtgaac tcttatttat ttttatgtat tccgttttat ttattttactg ccacgctact 1436  
 gataatcaga ccttcaatgat catccatctg gtgagcagag cttcatttgt atataacact 1496  
 ttcagagcct tcccacccat aggtagtct taaaccagggt gaaagagcaa agttcaagt 1556  
 cctacttatg tgtcattcgc tcatgtaaga gtttttaaga gagggctgat taccacagcc 1616  
 ctcttttctc ctgaattttt aatgcagaag ttggaatgaa gcaagggaag gcatgtagg 1676  
 acaggaaagg aaacaalga aggaaagtga ttctgtgaaa aggacagtga agccagctat 1736  
 ttaccceca ggctggattt tttttttttt tttttttttt ttttttttta ccgagtacac 1796  
 agagiacca agtgaagaga acgtcatgag tgtaagtga aatcagtga aggagcggca 1856  
 aactgggaca tgcagaattg aatttgcica aaaaaaaaaa aaaaa 1901

<210> 74

<211> 319

<212> PRT

<213> Homo sapiens

<400> 74

Met Met Val Leu Lys Val Glu Glu Leu Val Thr Gly Lys Lys Asn Gly

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20	25	30	
Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys Thr Leu			
35	40	45	
Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser Glu Lys			
50	55	60	
Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg Ser Lys			
65	70	75	80
Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys Lys Arg			
85	90	95	
Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro Glu Pro			
100	105	110	
Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys Ala Ala			
115	120	125	
Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp Lys Asn			
130	135	140	
Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His Arg Ala			
145	150	155	160
Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu Ala Gly			
165	170	175	
Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile His Trp			
180	185	190	
Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu Asn Lys			
195	200	205	
Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala Leu His			
210	215	220	

Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu Ile Ala

225 230 235 240

Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr Pro Leu

245 250 255

His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu Leu Ile

260 265 270

Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys Thr Pro

275 280 285

Met Asp Leu Val Leu His Trp Gln Asn Gly Thr Lys Ala Ile Phe Asp

290 295 300

Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr Phe

305 310 315

<210> 75

<211> 5613

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118).. (5475)

<400> 75

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ctcggcgggc gtcttctcca ctctctgcc gcgtccccgt ggctgcaggg agccggc 117

atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta gcc ctg tgc aga 165

Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg

1 5 10 15

gcc cga gtg cgc gct cag gaa ccc gag ttc agc tac ggc tgc gca gaa 213



Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu  
                   20                                  25                                  30  
 ggc agc tgc tat ccc gcc acg ggc gac ctt ctc atc ggc cga gca cag 261  
 Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln  
                   35                                  40                                  45  
 aag ctt tcg gtg acc tcg acg tgc ggg ctg cac aag ccc gaa ccc tac 309  
 Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr  
                   50                                  55                                  60  
 tgt atc gtc agc cac ttg cag gag gac aaa aaa tgc ttc ata tgc aat 357  
 Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn  
                   65                                  70                                  75                                  80  
 tcc caa gat cct tat cat gag acc ctg aat cct gac agc cat ctc att 405  
 Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile  
                   85                                  90                                  95  
 gaa aat gtg gtc act aca ttt gct cca aac cgc ctt aag att tgg tgg 453  
 Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp  
                   100                                  105                                  110  
 caa tct gaa aat ggt gtg gaa aat gta act atc caa ctg gat ttg gaa 501  
 Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu  
                   115                                  120                                  125  
 gca gaa ttc cat ttt act cat ctc ata atg act ttc aag aca ttc cgt 549  
 Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg  
                   130                                  135                                  140  
 cca gct gct atg ctg ata gaa cga tcg tcc gac ttt ggg aaa acc tgg 597  
 Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp  
                   145                                  150                                  155                                  160

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ggt gtg tat aga tac ttc gcc tat gac tgt gag gcc tgc ttt cca ggc 645
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
      165              170              175

att tca act ggc ccc atg aaa aaa gtc gat gac ata att tgt gat tct 693
Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
      180              185              190

cga tat tct gac att gaa ccc tca act gaa gga gag gtg ata ttt cgt 741
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
      195              200              205

gct tta gat cct gct ttc aaa ata gaa gat cct tat agc cca agg ata 789
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
      210              215              220

cag aat tta tta aaa att acc aac ttg aga atc aag ttt gtg aaa ctg 837
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
      225              230              235              240

cat act ttg gga gat aac ctt ctg gat tcc agg atg gaa atc aga gaa 885
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
      245              250              255

aag tat tat tat gca gtt tat gat atg gtg gtt cga gga aat tgc ttc 933
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
      260              265              270

tgc tat ggt cat gcc agc gaa tgt gcc cct gtg gat gga ttc aat gaa 981
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu
      275              280              285

gaa gtg gaa gga atg gtt cac gga cac tgc atg tgc agg cat aac acc 1029
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
      290              295              300

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aag ggc tta aac tgt gaa ctc tgc atg gat ttc tac cat gat tta cct 1077
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305          310          315          320
tgg aga cct gct gaa ggc cga aac agc aac gcc tgt aaa aaa tgt aac 1125
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
          325          330          335
tgc aat gaa cat tcc atc tct tgt cac ttt gac atg gct gtt tac ctg 1173
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu
          340          345          350
gcc acg ggg aac gtc agc gga ggc gtg tgt gat gac tgt cag cac aac 1221
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn
          355          360          365
acc atg ggg cgc aac tgt gag cag tgc aag ccg ttt tac tac cag cac 1269
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His
          370          375          380
cca gag agg gac atc cga gat cct aat ttc tgt gaa cga tgt acg tgt 1317
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys
385          390          395          400
gac cca gct ggc tct caa aat gag gga att tgt gac agc tat act gat 1365
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp
          405          410          415
ttt tct act ggt ctc att gct ggc cag tgt cgg tgt aaa tta aat gtg 1413
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val
          420          425          430
gaa gga gaa cat tgt gat gtt tgc aaa gaa ggc ttc tat gat tta agc 1461
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser

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435	440	445	
agt gaa gat cca ttt ggt tgt aaa tct tgt gct tgc aat cct ctg gga	1509		
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly			
450	455	460	
aca att cct gga ggg aat cct tgt gat tcc gag aca ggt cac tgc tac	1557		
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr			
465	470	475	480
tgc aag cgt ctg gtg aca gga cag cat tgt gac cag tgc ctg cca gag	1605		
Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu			
485	490	495	
cac tgg ggc tta agc aat gat ttg gat gga tgt cga cca tgt gac tgt	1653		
His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys			
500	505	510	
gac ctt ggg gga gcc tta aac aac agt tgc ttt gcg gag tca ggc cag	1701		
Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln			
515	520	525	
tgc tca tgc cgg cct cac atg att gga cgt cag tgc aac gaa gtg gaa	1749		
Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu			
530	535	540	
cct ggt tac tac ttt gcc acc ctg gat cac tac ctc tat gaa gcg gag	1797		
Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu			
545	550	555	560
gaa gcc aac ttg ggg cct ggg gtt agc ata gtg gag cgg caa tat atc	1845		
Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile			
565	570	575	
cag gac cgg att ccc tcc tgg act gga gcc ggc ttc gtc cga gtg cct	1893		
Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro			

580	585	590	
gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca tat tcc atg			1941
Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met			
595	600	605	
gag tac gac atc cta att cgc tac gag cca cag cta ccc gac cac tgg			1989
Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp			
610	615	620	
gaa aaa gct gtc atc aca gtg cag cga cct gga agg att cca acc agc			2037
Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser			
625	630	635	640
agc cga tgt ggt aat acc atc ccc gat gat gac aac cag gtg gtg tca			2085
Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser			
645	650	655	
tta tca cca ggc tca aga tat gtc gtc ctt cct cgg ccg gtg tgc ttt			2133
Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe			
660	665	670	
gag aag gga aca aac tac acg gtg agg ttg gag ctg cct cag tac acc			2181
Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr			
675	680	685	
tcc tct gat agc gac gtg gag agc ccc tac acg ctg atc gat tct ctt			2229
Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu			
690	695	700	
gtt ctc atg cca tac tgt aaa tca ctg gac atc ttc acc gtg gga ggt			2277
Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly			
705	710	715	720
tca gga gat ggg gtg gtc acc aac agt gcc tgg gaa acc ttt cag aga			2325

Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg  
 725 730 735  
 tac cga tgt cta gag aac agc aga agc gtt gtg aaa aca ccg atg aca 2373  
 Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr  
 740 745 750  
 gat gtt tgc aga aac atc atc ttt agc att tct gcc ctg tta cac cag 2421  
 Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln  
 755 760 765  
 aca ggc ctg gct tgt gaa tgc gac cct cag ggt tgc tta agt tcc gig 2469  
 Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val  
 770 775 780  
 tgt gat ccc aac gga ggc cag tgc cag tgc cgg ccc aac gtg gtt gga 2517  
 Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly  
 785 790 795 800  
 aga acc tgc aac aga tgt gca cct gga act ttt ggc ttt ggc ccc agt 2565  
 Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser  
 805 810 815  
 gga tgc aaa cct tgt gag tgc cat ctg caa gga tct gtc aat gcc ttc 2613  
 Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe  
 820 825 830  
 tgc aat ccc gtc act ggc cag tgc cac tgt ttc cag gga gtg tat gct 2661  
 Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala  
 835 840 845  
 cgg cag tgt gat cgg tgc tta cct ggg cac tgg ggc ttt cca agt tgc 2709  
 Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys  
 850 855 860  
 cag ccc tgc cag tgc aat ggc cac gcc gat gac tgc gac cca gtg act 2757

Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr  
 865                      870                      875                      880  
 ggg gag tgc ttg aac tgc cag gac tac acc atg ggt cat aac tgt gaa 2805  
 Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu  
                     885                      890                      895  
 agg tgc ttg gct ggt tac tat ggc gac ccc atc att ggg tca ggt gat 2853  
 Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp  
                     900                      905                      910  
 cac tgc cgc cct tgc cct tgc cca gat ggt ccc gac agt gga cgc cag 2901  
 His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln  
                     915                      920                      925  
 ttt gcc agg agc tgc tac caa gat cct gtt act tta cag ctt gcc tgt 2949  
 Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys  
                     930                      935                      940  
 gtt tgt gat cct gga tac att ggt tcc aga tgt gac gac tgt gcc tca 2997  
 Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser  
 945                      950                      955                      960  
 gga tac ttt ggc aat cca tca gaa gtt ggg ggg tcg tgt cag cct tgc 3045  
 Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys  
                     965                      970                      975  
 cag tgt cac aac aac att gac acg aca gac cca gaa gcc tgt gac aag 3093  
 Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys  
                     980                      985                      990  
 gag act ggg agg tgt ctc aag tgc ctg tac cac acg gaa ggg gaa cac 3141  
 Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His  
                     995                      1000                      1005

tgt cag ttc tgc cgg ttt gga tac tat ggt gat gcc ctc cgg cag gac 3189  
 Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp  
 1010 1015 1020  
 tgt cga aag tgt gtc tgt aat tac ctg ggc acc gtg caa gag cac tgt 3237  
 Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys  
 1025 1030 1035 1040  
 aac ggc tct gac tgc cag tgc gac aaa gcc act ggt cag tgc ttg tgt 3285  
 Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys  
 1045 1050 1055  
 ctt cct aat gtg atc ggg cag aac tgt gac cgc tgt gcg ccc aat acc 3333  
 Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr  
 1060 1065 1070  
 tgg cag ctg gcc agt ggc act ggc tgt gac cca tgc aac tgc aat gct 3381  
 Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala  
 1075 1080 1085  
 gct cat tcc ttc ggg cca tct tgc aat gag ttc acg ggg cag tgc cag 3429  
 Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln  
 1090 1095 1100  
 tgc atg cct ggg ttt gga ggc cgc acc tgc agc gag tgc cag gaa ctc 3477  
 Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu  
 1105 1110 1115 1120  
 ttc tgg gga gac ccc gac gtg gag tgc cga gcc tgt gac tgt gac ccc 3525  
 Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro  
 1125 1130 1135  
 agg ggc att gag acg cca cag tgt gac cag tcc acg ggc cag tgt gtc 3573  
 Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val  
 1140 1145 1150



tgc gtt gag ggt gtt gag ggt cca cgc igt gac aag tgc acg cga ggg 3621  
 Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly  
 1155 1160 1165  
 tac tcg ggg gtc ttc cct gac tgc aca ccc tgc cac cag tgc ttt gct 3669  
 Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala  
 1170 1175 1180  
 ctg tgg gat gtg atc att gcc gag ctg acc aac agg aca cac aga ttc 3717  
 Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe  
 1185 1190 1195 1200  
 ctg gag aaa gcc aag gcc ttg aag atc agt ggt gtg atc ggg cct tac 3765  
 Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr  
 1205 1210 1215  
 cgt gag act gtg gac tcg gtg gag agg aaa gtc agc gag ata aaa gac 3813  
 Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp  
 1220 1225 1230  
 atc ctg gcg cag agc ccc gca gca gag cca ctg aaa aac att ggg aat 3861  
 Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn  
 1235 1240 1245  
 ctg ttt gag gaa gca gag aaa ctg att aaa gat gtt aca gaa atg atg 3909  
 Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met  
 1250 1255 1260  
 gct caa gta gaa gtg aaa tta tct gac aca act tcc caa agc aac agc 3957  
 Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser  
 1265 1270 1275 1280  
 aca gcc aaa gaa ctg gat tct cta cag aca gaa gcc gaa agc cta gac 4005  
 Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp

1285 1290 1295  
aac act gtg aaa gaa ctt gct gaa caa ctg gaa ttt atc aaa aac tca 4053  
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser

1300 1305 1310  
gat att cgg ggt gcc ttg gat agc att acc aag tat ttc cag atg tct 4101  
Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser

1315 1320 1325  
ctt gag gca gag gag agg gtg aat gcc tcc acc aca gaa ccc aac agc 4149  
Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser

1330 1335 1340  
act gtg gag cag tca gcc ctc atg aga gac aga gta gaa gac gtg atg 4197  
Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met

1345 1350 1355 1360  
atg gag cga gaa tcc cag ttc aag gaa aaa caa gag gag cag gct cgc 4245  
Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg

1365 1370 1375  
ctc ctt gat gaa ctg gca ggc aag cta caa agc cta gac ctt tca gcc 4293  
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala

1380 1385 1390  
gct gcc gaa atg acc tgt gga aca ccc cca ggg gcc tcc tgt tcc gag 4341  
Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu

1395 1400 1405  
act gaa tgt ggc ggg cca aac tgc aga act gac gaa gga gag agg aag 4389  
Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys

1410 1415 1420  
tgt ggg ggg cct ggc tgt ggt ggt ctg gtt act gtt gca cac aac gcc 4437  
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala

1425                      1430                      1435                      1440  
 tgg cag aaa gcc atg gac ttg gac caa gat gtc ctg agt gcc ctg gct 4485  
 Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala  
                          1445                      1450                      1455  
 gaa gtg gaa cag ctc tcc aag atg gtc tct gaa gca aaa ctg agg gca 4533  
 Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala  
                          1460                      1465                      1470  
 gat gag gca aaa caa agt gct gaa gac att ctg ttg aag aca aat gct 4581  
 Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala  
                          1475                      1480                      1485  
 acc aaa gaa aaa atg gac aag agc aat gag gag ctg aga aat cta atc 4629  
 Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile  
                          1490                      1495                      1500  
 aag caa atc aga aac ttt ttg acc cag gat agt gct gat ttg gac agc 4677  
 Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser  
 1505                      1510                      1515                      1520  
 att gaa gca gtt gct aat gaa gta ttg aaa atg gag atg cct agc acc 4725  
 Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr  
                          1525                      1530                      1535  
 cca cag cag tta cag aac ttg aca gaa gat ata cgt gaa cga gtt gaa 4773  
 Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu  
                          1540                      1545                      1550  
 agc ctt tct caa gta gag gtt att ctt cag cat agt gct gct gac att 4821  
 Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile  
                          1555                      1560                      1565  
 gcc aga gct gag atg ttg tta gaa gaa gct aaa aga gca agc aaa agt 4869

Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser  
1570 1575 1580  
gca aca gat gtt aaa gtc act gca gat atg gta aag gaa gct ctg gaa 4917  
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu  
1585 1590 1595 1600  
gaa gca gaa aag gcc cag gtc gca gca gag aag gca att aaa caa gca 4965  
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala  
1605 1610 1615  
gat gaa gac att caa gga acc cag aac ctg tta act tcg att gag tct 5013  
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser  
1620 1625 1630  
gaa aca gca gct tct gag gaa acc ttg ttc aac gcg tcc cag cgc atc 5061  
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile  
1635 1640 1645  
agc gag tta gag agg aat gtg gaa gaa ctt aag cgg aaa gct gcc caa 5109  
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln  
1650 1655 1660  
aac tcc ggg gag gca gaa tat att gaa aaa gta gta tat act gtg aag 5157  
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys  
1665 1670 1675 1680  
caa agt gca gaa gat gtt aag aag act tta gat ggt gaa ctt gat gaa 5205  
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu  
1685 1690 1695  
aag tat aaa aaa gta gaa aat tta att gcc aaa aaa act gaa gag tca 5253  
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser  
1700 1705 1710  
gct gat gcc aga agg aaa gcc gaa atg cta caa aat gaa gca aaa act 5301

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Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr  
 1715 1720 1725  
 ctt tta gct caa gca aat agc aag ctg caa ctg ctc aaa gat tta gaa 5349  
 Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu  
 1730 1735 1740  
 aga aaa tat gaa gac aat caa aga tac tta gaa gat aaa gct caa gaa 5397  
 Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu  
 1745 1750 1755 1760  
 tta gca aga ctg gaa gga gaa gtc cgt tca ctc cta aag gat ata agc 5445  
 Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser  
 1765 1770 1775  
 cag aaa gtt gct gig tat agc aca tgc ttg taacagagga gaataaaaaa 5495  
 Gln Lys Val Ala Val Tyr Ser Thr Cys Leu  
 1780 1785  
 tggctgaggt gaacaaggta aaacaactac attttaaaaa ctgacttaat gctcttcaaa 5555  
 ataaaaacatc acctatitaa tgtttttaat cacattttgt atgagttaaa taaagccc 5613

&lt;210&gt; 76

&lt;211&gt; 1786

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg

1 5 10 15

Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu

20 25 30

Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln

35	40	45	
Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr			
50	55	60	
Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn			
65	70	75	80
Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile			
85	90	95	
Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp			
100	105	110	
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu			
115	120	125	
Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg			
130	135	140	
Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp			
145	150	155	160
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly			
165	170	175	
Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser			
180	185	190	
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg			
195	200	205	
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile			
210	215	220	
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu			
225	230	235	240
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu			

	245	250	255
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe			
260	265	270	
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu			
275	280	285	
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr			
290	295	300	
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro			
305	310	315	320
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn			
325	330	335	
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu			
340	345	350	
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn			
355	360	365	
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His			
370	375	380	
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys			
385	390	395	400
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp			
405	410	415	
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val			
420	425	430	
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser			
435	440	445	
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly			
450	455	460	

Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr  
 465                      470                      475                      480  
 Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu  
                     485                      490                      495  
 His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys  
                     500                      505                      510  
 Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln  
                     515                      520                      525  
 Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu  
                     530                      535                      540  
 Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu  
 545                      550                      555                      560  
 Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile  
                     565                      570                      575  
 Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro  
                     580                      585                      590  
 Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met  
                     595                      600                      605  
 Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp  
                     610                      615                      620  
 Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser  
 625                      630                      635                      640  
 Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser  
                     645                      650                      655  
 Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe  
                     660                      665                      670



Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr  
 675 680 685  
 Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu  
 690 695 700  
 Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly  
 705 710 715 720  
 Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg  
 725 730 735  
 Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr  
 740 745 750  
 Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln  
 755 760 765  
 Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val  
 770 775 780  
 Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly  
 785 790 795 800  
 Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser  
 805 810 815  
 Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe  
 820 825 830  
 Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala  
 835 840 845  
 Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys  
 850 855 860  
 Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr  
 865 870 875 880  
 Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu

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	885	890	895
Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp			
	900	905	910
His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln			
	915	920	925
Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys			
	930	935	940
Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser			
	945	950	955
Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys			960
	965	970	975
Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys			
	980	985	990
Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His			
	995	1000	1005
Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp			
	1010	1015	1020
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys			
	1025	1030	1035
Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys			1040
	1045	1050	1055
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr			
	1060	1065	1070
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala			
	1075	1080	1085
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln			

1090	1095	1100	
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu			
1105	1110	1115	1120
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro			
1125	1130	1135	
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val			
1140	1145	1150	
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly			
1155	1160	1165	
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala			
1170	1175	1180	
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe			
1185	1190	1195	1200
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr			
1205	1210	1215	
Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp			
1220	1225	1230	
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn			
1235	1240	1245	
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met			
1250	1255	1260	
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser			
1265	1270	1275	1280
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp			
1285	1290	1295	
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser			
1300	1305	1310	

Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser  
 1315 1320 1325  
 Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser  
 1330 1335 1340  
 Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met  
 1345 1350 1355 1360  
 Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg  
 1365 1370 1375  
 Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala  
 1380 1385 1390  
 Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu  
 1395 1400 1405  
 Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys  
 1410 1415 1420  
 Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala  
 1425 1430 1435 1440  
 Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala  
 1445 1450 1455  
 Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala  
 1460 1465 1470  
 Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala  
 1475 1480 1485  
 Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile  
 1490 1495 1500  
 Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser  
 1505 1510 1515 1520

Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr

1525

1530

1535

Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu

1540

1545

1550

Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile

1555

1560

1565

Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser

1570

1575

1580

Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu

1585

1590

1595

1600

Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala

1605

1610

1615

Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser

1620

1625

1630

Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile

1635

1640

1645

Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln

1650

1655

1660

Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys

1665

1670

1675

1680

Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu

1685

1690

1695

Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser

1700

1705

1710

Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr

1715

1720

1725

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu

[illegible]

&lt;210&gt; 77

<211> 585

&lt;212&gt; DNA

<213> Homo sapiens

<220>

&lt;221&gt; CDS

<222> (27) .. (335)

&lt;400&gt; 77

ctgagactga cctgcaggac gaaacc atg aag agc ctg atc ctt ctt gcc atc 53

Met Lys Ser Leu Ile Leu Leu Ala Ile

1 5

ctg gcc gcc tta gcg gta gta act ttg tgt tat gaa tca cat gaa agc 101

Leu Ala Ala Leu Ala Val Val Thr Leu Cys Tyr Glu Ser His Glu Ser

10 15 20 25

atg gaa tct tat gaa ctt aat ccc ttc att aac agg aga aat gca aat 149

Met Glu Ser Tyr Glu Leu Asn Pro Phe Ile Asn Arg Arg Asn Ala Asn

30                      35                      40

acc ttc ata tcc cct cag cag aga tgg aga gct aaa gtc caa gag agg 197

Thr Phe Ile Ser Pro Gln Gln Arg Trp Arg Ala Lys Val Gln Glu Arg

45 50 55  
 atc cga gaa cgc tct aag cct gtc cac gag ctc aat agg gaa gcc tgt 245  
 Ile Arg Glu Arg Ser Lys Pro Val His Glu Leu Asn Arg Glu Ala Cys  
 60 65 70  
 gat gac tac aga ctt tgc gaa cgc tac gcc atg gtt tat gga tac aat 293  
 Asp Asp Tyr Arg Leu Cys Glu Arg Tyr Ala Met Val Tyr Gly Tyr Asn  
 75 80 85  
 gct gcc tat aat cgc tac ttc agg aag cgc cga ggg acc aaa 335  
 Ala Ala Tyr Asn Arg Tyr Phe Arg Lys Arg Arg Gly Thr Lys  
 90 95 100  
 tgagactgag ggaagaaaaa aaatctcttt ttctctggag gctggcacct gattttgtat 395  
 cccctgttag cagcattact gaaatacata ggcttatata caatgcttct ttctgtata 455  
 ttctcttgtc tggctgcacc cctttttccc gccccagat tgataagtaa tgaaagtga 515  
 ctgcagtgag ggtcaaagga gagtcaacat aigtgattgt tccataataa acttctgggtg 575  
 tgatactttc 585

&lt;210&gt; 78

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 78

Met Lys Ser Leu Ile Leu Leu Ala Ile Leu Ala Ala Leu Ala Val Val

1

5

10

15

Thr Leu Cys Tyr Glu Ser His Glu Ser Met Glu Ser Tyr Glu Leu Asn

20

25

30

Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln

35

40

45

Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro

50

55

60

Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu

65

70

75

80

Arg Tyr Ala Met Val Tyr Gly Tyr Asn Ala Ala Tyr Asn Arg Tyr Phe

85

90

95

Arg Lys Arg Arg Gly Thr Lys

100

<210> 79

<211> 1775

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6).. (1148)

<400> 79

cagca atg cat ctc ctt gcg att ctg ttt tgt gct ctc tgg tct gca gtg 50

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val

1

5

10

15

ttg gcc gag aac tcg gat gat tat gat ctc atg tat gtg aat ttg gac 98

Leu Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp

20

25

30

aac gaa ata gac aat gga ctc cat ccc act gag gac ccc acg ccg tgc 146

Asn Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys

35

40

45

gcc tgc ggt cag gag cac tcg gaa tgg gac aag ctc ttc atc atg ctg 194



Ala Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu  
 50 55 60  
 gag aac tcg cag atg aga gag cgc atg ctg ctg caa gcc acg gac gac 242  
 Glu Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp  
 65 70 75  
 gtc ctg cgg ggc gag ctg cag agg ctg cgg gag gag ctg ggc cgg ctc 290  
 Val Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu  
 80 85 90 95  
 gcg gaa agc ctg gcg agg ccg tgc gcg ccg ggg gct ccc gca gag gcc 338  
 Ala Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala  
 100 105 110  
 agg ctg acc agt gct ctg gac gag ctg ctg cag gcg acc cgc gac gcg 386  
 Arg Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala  
 115 120 125  
 ggc cgc agg ctg gcg cgt atg gag ggc gcg gag gcg cag cgc cca gag 434  
 Gly Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu  
 130 135 140  
 gag gcg ggg cgc gcc ctg gcc gcg gtg cta gag gag ctg cgg cag acg 482  
 Glu Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr  
 145 150 155  
 cga gcc gac ctg cac gcg gtg cag ggc tgg gct gcc cgg agc tgg ctg 530  
 Arg Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu  
 160 165 170 175  
 ccg gca ggt tgt gaa aca gct att tta ttc cca atg cgt tcc aag aag 578  
 Pro Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys  
 180 185 190

att ttt gga agc gtg cat cca gtg aga cca atg agg ctt gag tct ttt 626  
 Ile Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe  
 195 200 205  
 agt gcc tgc att tgg gtc aaa gcc aca gat gta tta aac aaa acc atc 674  
 Ser Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile  
 210 215 220  
 ctg ttt tcc tat ggc aca aag agg aat cca tat gaa atc cag ctg tat 722  
 Leu Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr  
 225 230 235  
 ctc agc tac caa tcc ata gtg ttt gtg gtg ggt gga gag gag aac aaa 770  
 Leu Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys  
 240 245 250 255  
 ctg gtt gct gaa gcc atg gtt tcc ctg gga agg tgg acc cac ctg tgc 818  
 Leu Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys  
 260 265 270  
 ggc acc tgg aat tca gag gaa ggg ctc aca tcc ttg tgg gta aat ggt 866  
 Gly Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly  
 275 280 285  
 gaa ctg gcg gct acc act gtt gag atg gcc aca ggt cac att gtt cct 914  
 Glu Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro  
 290 295 300  
 gag gga gga atc ctg cag att ggc caa gaa aag aat ggc tgc tgt gtg 962  
 Glu Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val  
 305 310 315  
 ggt ggt ggc ttt gat gaa aca tta gcc ttc tct ggg aga ctc aca ggc 1010  
 Gly Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly  
 320 325 330 335

ttc aat atc tgg gat agt gtt ctt agc aat gaa gag ata aga gag acc 1058  
 Phe Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr

340

345

350

gga gga gca gag tct tgt cac atc cgg ggg aat att gtt ggg tgg gga 1106  
 Gly Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly

355

360

365

gtc aca gag atc cag cca cat gga gga gct cag tat gtt tca 1148  
 Val Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser

370

375

380

taaattgtgt gaaactccac ttgaagccaa agaaagaaac tcacacttaa aacacatgcc 1208  
 agttgggaag gtctgaaaac tcagtgcata ataggaacac ttgagactaa tgaaagagag 1268  
 agttgagacc aatctttatt tglactggcc aaatactgaa taaacagttg aaggaaagac 1328  
 attggaaaaa gcttttgagg ataattgttac tagactttat gccatgggtgc tttcagttta 1388  
 atgctgtgtc tctgtcagat aaactctcaa ataattaaaa aggacigtat tgttgaacag 1448  
 aggacaatt gttttacttt tctttggtta attttgtttt ggccagagat gaattttaca 1508  
 ttggaagaat aacaaaataa gatttgttgt ccattgttca ttgttatagg tatgtacctt 1568  
 attacaaaaa aaatgatgaa aacatattta tactacaagg tgacttaaca actataaatg 1628  
 tagtttaigt gttataatcg aatgtcacgt ttttgagaag atagtcatat aagttatatt 1688  
 gcaaaaggga tttgtattaa ttttaagacta tttttgtaaa gctctactgt aaataaaaata 1748  
 ttttataaaa ctaaaaaaaa aaaaaaa 1775

&lt;210&gt; 80

&lt;211&gt; 381

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 80

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val Leu

1	5	10	15
Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp Asn			
20	25	30	
Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys Ala			
35	40	45	
Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu Glu			
50	55	60	
Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp Val			
65	70	75	80
Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu Ala			
85	90	95	
Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala Arg			
100	105	110	
Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala Gly			
115	120	125	
Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu Glu			
130	135	140	
Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr Arg			
145	150	155	160
Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu Pro			
165	170	175	
Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys Ile			
180	185	190	
Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe Ser			
195	200	205	
Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile Leu			

210 215 220  
Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr Leu  
225 230 235 240  
Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys Leu  
245 250 255  
Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys Gly  
260 265 270  
Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly Glu  
275 280 285  
Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro Glu  
290 295 300  
Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val Gly  
305 310 315 320  
Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly Phe  
325 330 335  
Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr Gly  
340 345 350  
Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly Val  
355 360 365  
Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser  
370 375 380

&lt;210&gt; 81

&lt;211&gt; 2312

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (146).. (1192)

&lt;400&gt; 81

tccagtgacg gagccgcccc gccgacagcc ccgagacgac agccccggcgc gtccccgtcc 60  
 ccaccitccga ccaccgccag cgctccaggc cccgcgcctc ccgcctcgccg ccaccgcgcc 120  
 ctccgcctccg cccgcagtcg caacc atg acc gcc gcc agt atg ggc ccc gtc 172

Met Thr Ala Ala Ser Met Gly Pro Val

1

5

cgc gtc gcc ttc gtg gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc 220

Arg Val Ala Phe Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val

10

15

20

25

ggc cag aac tgc agc ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg 268

Gly Gln Asn Cys Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro

30

35

40

cgc tgc ccg gcg ggc gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc 316

Arg Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys

45

50

55

cgc gtc tgc gcc aag cag ctg ggc gag ctg tgc acc gag cgc gac ccc 364

Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro

60

65

70

tgc gac ccg cac aag ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac 412

Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn

75

80

85

cgc aag atc ggc gtg tgc acc gcc aaa gat ggt gct ccc tgc atc ttc 460

Arg Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe

90

95

100

105

ggt ggt acg gtg tac cgc agc gga gag tcc ttc cag agc agc tgc aag 508

Gly Gly Thr Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys  
 110 115 120  
 tac cag tgc acg tgc ctg gac ggg gcg glg ggc tgc atg ccc ctg tgc 556  
 Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys  
 125 130 135  
 agc atg gac gtt cgt ctg ccc agc cct gac tgc ccc ttc ccg agg agg 604  
 Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg  
 140 145 150  
 gtc aag ctg ccc ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc 652  
 Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro  
 155 160 165  
 aag gac caa acc glg gtt ggg cct gcc ctc gcg gct tac cga ctg gaa 700  
 Lys Asp Gln Thr Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu  
 170 175 180 185  
 gac acg ttt ggc cca gac cca act atg att aga gcc aac tgc ctg gtc 748  
 Asp Thr Phe Gly Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val  
 190 195 200  
 cag acc aca gag tgg agc gcc tgt tcc aag acc tgt ggg atg ggc atc 796  
 Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile  
 205 210 215  
 tcc acc cgg gtt acc aat gac aac gcc tcc tgc agg cta gag aag cag 844  
 Ser Thr Arg Val Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln  
 220 225 230  
 agc cgc ctg tgc atg gtc agg cct tgc gaa gct gac ctg gaa gag aac 892  
 Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn  
 235 240 245

att aag aag ggc aaa aag tgc atc cgt act ccc aaa atc tcc aag cct 940  
 Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro  
 250 255 260 265  
 atc aag ttt gag ctt tct ggc tgc acc agc atg aag aca tac cga gct 988  
 Ile Lys Phe Glu Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala  
 270 275 280  
 aaa ttc tgt gga gla tgt acc gac ggc cga tgc tgc acc ccc cac aga 1036  
 Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg  
 285 290 295  
 acc acc acc ctg ccg gtg gag ttc aag tgc cct gac ggc gag gtc atg 1084  
 Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met  
 300 305 310  
 aag aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt 1132  
 Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys  
 315 320 325  
 ccc gga gac aat gac atc ttt gaa tcg ctg tac tac agg aag atg tac 1180  
 Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr  
 330 335 340 345  
 gga gac atg gca tgaagccaga gaggagaga cattaactca ttagactgga 1232  
 Gly Asp Met Ala  
 acttgaactg attcacatct ctttttccg taaaaatgat ttcagtagca caagtatttt 1292  
 aaatctgttt ttctaactgg gggaaaagat tcccacccaa ttcaaaacat tgtgcatgt 1352  
 caaacaata gtctatcttc ccagacact gggttgaaga atgttaagac ttgacagtgg 1412  
 aactacatta gtacacagca ccagaatgta tattaaggig tggctttagg agcagtggga 1472  
 gggtaccagc agaaaggta gtatcatcag atagctctta tacgagtaat atgcttgcta 1532  
 ttigaagtgt aattgagaag gaaaatttta gcgtgctcac tgacctgcct gtagccccag 1592  
 tgacagctag gatgtgcatt ctccagccat caagagactg agtcaagttg ttccttaagt 1652



cagaacagca gactcagctc tgacattctg attcgaatga cactgttcag gaatcggaat 1712  
 ccctgctgatt agactggaca gcttgtggca agigaatttc ctgtaacaag ccagattttt 1772  
 taaaattttat attgtaaata ttgtgtgtgt gtgtgtgtgt giatatatat atatatatgt 1832  
 acagttaatct aagttaattt aaagttgttt gtgccttttt atttttgttt ttaatgcttt 1892  
 gatatttcaa tgitagccctc aatttctgaa caccataggt agaatgtaaa gcttgtctga 1952  
 tcgttcaaag catgaaatgg atacttataat ggaaattctc tcagatagaa tgacagtccg 2012  
 tcaaaacaga ttgtttgcaa aggggaggca tcagtgtcct tggcaggctg atttctaggt 2072  
 aggaaatgtg gtagctcacg ctacatttta atgaacaaat ggcctttatt aaaaactgag 2132  
 tgactctata tagctgatca gttttttcac ctggaagcat ttgtttctac tttgatatga 2192  
 ctgtttttcg gacagttaat ttgttgagag tgtgacaaaa agttacatgt ttgcaccttt 2252  
 ctagttgaaa ataaagtata ttttttctaa aaaaaaaaaa aaacgacagc aacggaattc 2312

<210> 82

<211> 349

<212> PRT

<213> Homo sapiens

<400> 82

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu

1 5 10 15

Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro

20 25 30

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser

35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu

50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu

65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr  
85 90 95  
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser  
100 105 110  
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp  
115 120 125  
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro  
130 135 140  
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys  
145 150 155 160  
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly  
165 170 175  
Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro  
180 185 190  
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala  
195 200 205  
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp  
210 215 220  
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg  
225 230 235 240  
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys  
245 250 255  
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly  
260 265 270  
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr  
275 280 285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu

290

295

300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile

305

310

315

320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe

325

330

335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala

340

345

&lt;210&gt; 83

&lt;211&gt; 2954

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (173).. (1525)

&lt;400&gt; 83

gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcagggag 60

ggcccagggc gccagggagg ccgcgccggg ctaatccgaa ggggctgcga ggicaggctg 120

taaccgggtc aatgtgtgga atatiggggg gctcggctgc agacttggcc aa atg gac 178

Met Asp

1

ggg act att aag gag gct ctg tgc gtg gtg agc gac gac cag tcc ctc 226

Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln Ser Leu

5

10

15

ttt gac tca gcg tac gga gcg gca gcc cat ctc ccc aag gcc gac atg 274

Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala Asp Met

20	25	30	
act gcc tgc ggg agt cct gac tac ggg cag ccc cac aag atc aac ccc	322		
Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile Asn Pro			
35	40	45	50
ctc cca cca cag cag gag tgg atc aat cag cca gtc agg gtc aac gtc	370		
Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val Asn Val			
55	60	65	
aag cgg gag tat gac cac atg aat gga tcc agg gag tct ccg gtc gac	418		
Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro Val Asp			
70	75	80	
tgc agc gtt agc aaa tgc agc aag ctg gtc ggc gga ggc gag tcc aac	466		
Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu Ser Asn			
85	90	95	
ccc atg aac tac aac agc tat atg gac gag aag aat ggc ccc cct cct	514		
Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro Pro Pro			
100	105	110	
ccc aac atg acc acc aac gag agg aga gtc atc gtc ccc gca gac ccc	562		
Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala Asp Pro			
115	120	125	130
aca ctg tgg aca cag gag cat gtc agg caa tgg ctg gag tgg gcc ata	610		
Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp Ala Ile			
135	140	145	
aag gag tac agc ttg atg gag atc gac aca tcc ttt ttc cag aac atg	658		
Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln Asn Met			
150	155	160	
gat ggc aag gaa ctg tgt aaa atg aac aag gag gac ttc ctc cgc gcc	706		
Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu Arg Ala			

165	170	175	
acc acc ctc tac aac acg gaa gtg ctg ttg tca cac ctc agt tac ctc	754		
Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser Tyr Leu			
180	185	190	
agg gaa agt tca ctg ctg gcc tat aat aca acc tcc cac acc gac caa	802		
Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr Asp Gln			
195	200	205	210
tcc tca cga ttg agt gtc aaa gaa gac cct tct tat gac tca gtc aga	850		
Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser Val Arg			
215	220	225	
aga gga gct tgg ggc aat aac atg aat tct ggc ctc aac aaa agt cct	898		
Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys Ser Pro			
230	235	240	
ccc ctt gga ggg gca caa acg atc agt aag aat aca gag caa cgg ccc	946		
Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln Arg Pro			
245	250	255	
cag cca gat ccg tat cag atc ctc ggc ccg acc agc agt cgc cta gcc	994		
Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala			
260	265	270	
aac cct gga agc ggg cag atc cag ctg tgg caa ttc ctc ctg gag ctg	1042		
Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu			
275	280	285	290
ctc tcc gac agc gcc aac gcc agc tgt atc acc tgg gag ggg acc aac	1090		
Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly Thr Asn			
295	300	305	
ggg gag ttc aaa atg acg gac ccc gat gag gtg gcc agg cgc tgg ggc	1138		

Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly  
 310 315 320  
 gag cgg aaa agc aag ccc aac atg aat tac gac aag ctg agc cgg gcc 1186  
 Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala  
 325 330 335  
 ctc cgt tat tac tat gat aaa aac att atg acc aaa gtg cac ggc aaa 1234  
 Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His Gly Lys  
 340 345 350  
 aga tat gct tac aaa ttt gac ttc cac ggc att gcc cag gct ctg cag 1282  
 Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala Leu Gln  
 355 360 365 370  
 cca cat ccg acc gag tcg tcc atg tac aag tac cct tct gac atc tcc 1330  
 Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp Ile Ser  
 375 380 385  
 tac atg cct tcc caa cat gcc cac cag cag aag gtg aac ttt gtc cct 1378  
 Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe Val Pro  
 390 395 400  
 ccc cat cca tcc tcc atg cct gtc act tcc tcc agc ttc ttt gga gcc 1426  
 Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe Gly Ala  
 405 410 415  
 gca tca caa tac tgg acc tcc acg ggg gga atc tac ccc aac ccc aac 1474  
 Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn Pro Asn  
 420 425 430  
 gtc ccc cgc cat cct aac acc cac gtg cct tca cac tta ggc agc tac 1522  
 Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly Ser Tyr  
 435 440 445 450  
 tac tagaagctta ctcatcagtg gccttctagc tgaagcccat cctgcacact 1575

Tyr

tactggatgc ttggactca acaggacata tgggccttg aaggaagac aaaactggat 1635  
gttctttctt gtggataga acccttgiat ttgttcttta aaaatatttt ttttaatgtt 1695  
gglaactttt gcttctctta cctgaacaaa gagatgaata attccaiggg ccagtatgcc 1755  
agtttgaatt ctcagctccc tagcatcttg tgagttgcat attaagatta ctggaatggt 1815  
taagtcattg ttctgagaaa gaagctgtac gttttcttta tgtttttatg accaaagcag 1875  
tttcttgtca atacacgggg ttcagtatga cacagaalca tggactaac ccgtcatggt 1935  
ctggtttgag atttagtgac aaatagaggt gggaagctta taatctaatt ttaggaggac 1995  
caaattcagc ggaatggcaac tggaaacttg attgtaaggc cagtgaagtt ttacccaac 2055  
tggaatttga tggaaagaag gtttgtgtgt ttaagacgcc aagggcattg cagaatccct 2115  
ctcagtggac agtatgcact cagctgacca ctctctctag aaalagtcaa gatatgaact 2175  
aagaaatttt aatgcaaata cataattcc tgaagacgg ggaattaaat tactaatttt 2235  
ttttttttaa atgatgacag tggctccaga acttggaaaa gtgttaggga ttctaaact 2295  
caagcagatt cgcaagtgct gtgcgcttgi cagaccatca gaccagggcc aaccaatcag 2355  
aaggcaactt actgtataaa ttatgcagag ttattttcct atatctcaca gtattaaaaa 2415  
ataaataatt aaaaattag aataaataaa cgagttgacc tcggtcacaa aagcagtttt 2475  
actatcgaat caatcgctgt tatttttttt taatgtaatt tglacatctt tttcaatct 2535  
gtacatttgg gctgtcttgt atgtttttat gctccttttt aaaaagcata atatgcctat 2595  
agctgaaaag gaaacagggc tglttaagtc actgacttat gagaaagcaa agcactggta 2655  
cagttattta acaggcatac acaagcaggg aaaagataat ccaattagat ctttaatgct 2715  
ttggaaatgc glgtaacagt actgcaataa tcacagctct gggaaaaaca acgaaacttt 2775  
cccttgtaga gaggaggat ttccctgctc tatataagca acatattttt agacattaaa 2835  
atatatataa ttttgcaggt aatgttgac ttttttaact atattaagtg ttaagctgac 2895  
aacgtcaaa gaagaccatg ttgtaaaata atttgactaa ataaatggtt ccttctctc 2954

&lt;210&gt; 84

&lt;211&gt; 451

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 84

Met Asp Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln

1

5

10

15

Ser Leu Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala

20

25

30

Asp Met Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile

35

40

45

Asn Pro Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val

50

55

60

Asn Val Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro

65

70

75

80

Val Asp Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu

85

90

95

Ser Asn Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro

100

105

110

Pro Pro Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala

115

120

125

Asp Pro Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp

130

135

140

Ala Ile Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln

145

150

155

160

Asn Met Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu

165

170

175

Arg Ala Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser



180	185	190	
Tyr Leu Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr			
195	200	205	
Asp Gln Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser			
210	215	220	
Val Arg Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys			
225	230	235	240
Ser Pro Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln			
245	250	255	
Arg Pro Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg			
260	265	270	
Leu Ala Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu			
275	280	285	
Glu Leu Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly			
290	295	300	
Thr Asn Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg			
305	310	315	320
Trp Gly Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser			
325	330	335	
Arg Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His			
340	345	350	
Gly Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala			
355	360	365	
Leu Gln Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp			
370	375	380	
Ile Ser Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe			
385	390	395	400

Val Pro Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe

405

410

415

Gly Ala Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn

420

425

430

Pro Asn Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly

435

440

445

Ser Tyr Tyr

450

&lt;210&gt; 85

&lt;211&gt; 1817

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2).. (361)

&lt;400&gt; 85

g cag cag gat ggg gag ggc cat acc cag gac acg gag ctc gtg gag acc 49

Gln Gln Asp Gly Glu Gly His Thr Gln Asp Thr Glu Leu Val Glu Thr

1

5

10

15

agg cct gca ggg gat gga acc ttc cag aag tgg gca gct gtg gtg gtg 97

Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val

20

25

30

cct tct gga gag gag cag aga tac acg tgc cat gtg cag cat gag ggg 145

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

35

40

45

cta ccc gag ccc gtc acc ctg aga tgg aag ccg gct tcc cag ccc acc 193

Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr  
 50 55 60  
 atc ccc aic gtg ggc atc att gct ggc ctg gtt ctc ctt gga tct gtg 241  
 Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val  
 65 70 75 80  
 gtc tct gga gct gtg gtt gct gct gtg ata tgg agg aag aag agc tca 289  
 Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser  
 85 90 95  
 ggt gga aaa gga ggg agc tac tct aag gct gag tgg agc gac agt gcc 337  
 Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala  
 100 105 110  
 cag ggg tct gag tct cac agc ttg taaagcctga gacagctgcc ttgtgtgcga 391  
 Gln Gly Ser Glu Ser His Ser Leu  
 115 120  
 ctgagatgca cagctgcctt gtgtgcgact gagatgcagg atttcctcac gcctccccta 451  
 tgtgtcttag gggactctgg ctctcttttt tgcaagggcc tctgaatctg tctgtgtccc 511  
 tgttagcaca atgtgaggag gtagagaaac agtccacctc tgtgtctacc atgaccccct 571  
 tcttcacact gacctgtgtt ccttcctgt tctcttttct attaaaaata agaacctggg 631  
 cagagtgcgg cagctcatgc ctgtaatccc agcacttagg gaggccgagg agggcagatc 691  
 acgaggtcag gagatcgaaa ccatacctggc taacacgggtg aaaccccgtc tctactaaaa 751  
 aatacaaaaa attagctggg cgcagaggca cgggcttgta glcccagcta ctcaggaggc 811  
 ggaggcagga gaatggcgtc aaccgggag gcggagggtg cagtgagcca ggattgtgcg 871  
 actgcatcca gcctgggtga cagggtgaaa cgccatctca aaaaataaaa attgaaaaat 931  
 aaaaaaagaa cctggatctc aatttaattt ttcatattct tgcaatgaaa tggacttgag 991  
 gaagctaaaga tcatagciag aaatacagat aattccacag cacatctctc gcaaatttag 1051  
 cctatticcta ttctciagcc tattccttac cacctgtaat ctgaccata taccttggag 1111

ttgaatatig ttttcalact gctgtggttt gaatgttccc tccaacacac atgttgagac 1171  
 ttaatcccta atgtggcaat acigaaaggt ggggcctttg agatlgatt ggatcgtaag 1231  
 gctgtgccctt cattcatggg ttaatggatt aatgggttat cacaggaatg ggactgggtg 1291  
 ctttataaga agaggaaaag agaactgagc tagcatgccc agcccacaga gagccctccac 1351  
 tagagtgatg ctaagtggaa atgtgaggtg cagctgccac agagggcccc caccagggaa 1411  
 atgtctagtg tctagtggat ccaggccaca ggagagagtg ccttgtggag cgctgggagc 1471  
 aggacctga accaccacca gaccccagaa ctgtggagtc agtggcagca tgcagcgccc 1531  
 ctigggaaag ctttagcacc agcctgcaac ccattcgacg agccacgtag gctgcacca 1591  
 gcaaagccac aggcacgggg ctacctgagc ctggggggcc caatccctgc tccagtgtgt 1651  
 ccgtgaggca gcacacgaag tcaaaagaga ttattctctt cccacagata ccttttctct 1711  
 cccatgacct tttaacagca tctgttcat tccctcacc tcccaggct gatctgaggt 1771  
 aaactttgaa gtaaaataaa agctgtgttt gagcatcaaa aaaaaa 1817

<210> 86

<211> 120

<212> PRT

<213> Homo sapiens

<400> 86

Gln Gln Asp Gly Glu Gly His Thr Gln Asp Thr Glu Leu Val Glu Thr

1 5 10 15

Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val

20 25 30

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

35 40 45

Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr

50 55 60

Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val

65                      70                      75                      80  
 Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser  
                          85                      90                      95  
 Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala  
                          100                      105                      110  
 Gln Gly Ser Glu Ser His Ser Leu  
                          115                      120

<210> 87

<211> 2876

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1281)

<400> 87

gaattccctgc agctcagcag ccgccgccag agcaggacga accgccaatc gcaaggcacc 60  
 tctgagaact tcagg atg cag atg tct cca gcc ctg acc tgc cta gtc ctg 111  
                          Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu  
                          1                      5                      10  
 ggc ctg gcc ctt gtc ttt ggt gaa ggg tct gct gtg cac cat ccc cca 159  
 Gly Leu Ala Leu Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro  
                          15                      20                      25  
 tcc tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag 207  
 Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln  
                          30                      35                      40  
 cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat 255

Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr  
 45 50 55 60  
 ggg gtg gcc tgc gtg ttg gcc atg ctc cag ctg aca aca gga gga gaa 303  
 Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu  
 65 70 75  
 acc cag cag cag att caa gca gct atg gga ttc aag att gat gac aag 351  
 Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys  
 80 85 90  
 ggc atg gcc ccc gcc ctc cgg cat ctg tac aag gag ctc atg ggg cca 399  
 Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro  
 95 100 105  
 tgg aac aag gat gag atc agc acc aca gac gcg atc ttc gtc cag cgg 447  
 Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg  
 110 115 120  
 gat ctg aag ctg gtc cag ggc ttc atg ccc cac ttc ttc agg ctg ttc 495  
 Asp Leu Lys Leu Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe  
 125 130 135 140  
 cgg agc acg gtc aag caa gtg gac ttt tca gag gtg gag aga gcc aga 543  
 Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg  
 145 150 155  
 ttc atc atc aat gac tgg gtg aag aca cac aca aaa ggt atg atc agc 591  
 Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser  
 160 165 170  
 aac ttg ctt ggg aaa gga gcc gtg gac cag ctg aca cgg ctg gtg ctg 639  
 Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu  
 175 180 185  
 gtg aat gcc ctc tac ttc aac ggc cag tgg aag act ccc ttc ccc gac 687

Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp  
 190 195 200  
 tcc agc acc cac cgc cgc ctc ttc cac aaa tca gac ggc agc act gtc 735  
 Ser Ser Thr His Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val  
 205 210 215 220  
 tct gtg ccc atg atg gct cag acc aac aag ttc aac tat act gag ttc 783  
 Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe  
 225 230 235  
 acc acg ccc gat ggc cat tac tac gac atc ctg gaa ctg ccc tac cac 831  
 Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His  
 240 245 250  
 ggg gac acc ctc agc atg ttc att gct gcc cct tat gaa aaa gag gtg 879  
 Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val  
 255 260 265  
 cct ctc tct gcc ctc acc aac att ctg agt gcc cag ctc atc agc cac 927  
 Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His  
 270 275 280  
 tgg aaa ggc aac atg acc agg ctg ccc cgc ctc ctg gtt ctg ccc aag 975  
 Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys  
 285 290 295 300  
 ttc tcc ctg gag act gaa gtc gac ctc agg aag ccc cta gag aac ctg 1023  
 Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu  
 305 310 315  
 gga atg acc gac atg ttc aga cag ttt cag gct gac ttc acg agt ctt 1071  
 Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu  
 320 325 330

tca gac caa gag cct ctc cac gtc gcg cag gcg ctg cag aaa gtg aag 1119

Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys

335

340

345

atc gag gig aac gag agt ggc acg gtg gcc tcc tca tcc aca gct gtc 1167

Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val

350

355

360

ata gtc tca gcc cgc atg gcc ccc gag gag atc atc atg gac aga ccc 1215

Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro

365

370

375

380

ttc ctc ttt gtg gtc cgg cac aac ccc aca gga aca gtc ctt ttc atg 1263

Phe Leu Phe Val Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met

385

390

395

ggc caa gtg atg gaa ccc tgacctggg gaaagacgcc ttcactggg 1311

Gly Gln Val Met Glu Pro

400

acaaaacigg agatgcatcg ggaaagaaga aaticcgaag aaaagaattt tagtgitaat 1371

gactctttct gaaggaagag aagacatttg ccttttgta aaagatggta aaccagatct 1431

gtctccaaga ccttggcctc tccttggagg accttaggt caaacccct agtctccacc 1491

tgagaccttg ggagagaagt ttgaagcaca actcccttaa ggtctccaaa ccagacgggtg 1551

acgcctgcgg gacctctgg ggcacctgct tccaccgctc tctctgcca ctcgggtctg 1611

cagacctggt tcccactgag gccctttgca ggaiggaact acggggctta caggagcttt 1671

tgtgtgcttg gtagaaacta tttctgttcc agtcacattg ccatcactct tgtactgcct 1731

gccaccgcgg aggaggcttg tgacaggcca aaggccagtg gaagaaacac cttttcalct 1791

cagagtccac tgtggcactg gccaccctc cccagtacag gggctctgca ggtggcagag 1851

tgaatgtccc ccatcatgtg gcccaactct cctggccctg ccatctccct cccagaaac 1911

agtgctcalt ggttattttg gagttaggt gacttgltta ctcatgaag cagatttctg 1971

cttcctttta tttttatagg aatagaggaa gaaatgtcag atgcgtgccc agctcttcac 2031



cccccaatct cttgggtggg aggggigtac ctaaataitt atcatatcct tgccttgag 2091  
 tgccttgtag agagaaagag aactactaag gaaaataata ttatttaaac tcgctcctag 2151  
 tgtttctttg tggctcgtgt caccglatct caggaagtc agccacttga ctggcacaca 2211  
 cccctccgga catccagcgt gacggagccc aactgccac ctigtggccg cctgagacc 2271  
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 ttcatccct cttcagggga tcaaaaggac ggagtggggg gacagagact cagatgagga 2391  
 cagagtgggt tccaatgtgt tcaatagatt taggagcaga aatgcaagg gctgcatgac 2451  
 ctaccaggac agaactttcc ccaattacag ggtgactcac agccgcattg gtgactcact 2511  
 tcaatgtgtc atttccggct gctgtgtgtg agcagtggac acgtgagggg ggggtgggtg 2571  
 agagagacag gcagctcgga ttcaactacc ttagataata tttctgaaaa cctaccagcc 2631  
 agagggtagg gcacaaagat ggatgtaatg cactttggga ggccaaggcg ggaggattgc 2691  
 ttgagcccag gattcaaga ccagcctggg caacatacca agacccccgt ctttttaaaa 2751  
 atatataat tttaaatata cttaaatata ttttctaata atctttaaat atatataat 2811  
 attttaaaga ccaatttatg ggagaattgc acacagatgt gaaatgaatg taatctaata 2871  
 gaagc 2876

<210> 88

<211> 402

<212> PRT

<213> Homo sapiens

<400> 88

Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu  
 Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala  
 1 5 10 15  
 His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln  
 20 25 30  
 Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser

35	40	45	
Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln			
50	55	60	
Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro			
65	70	75	80
Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp			
85	90	95	
Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu			
100	105	110	
Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val			
115	120	125	
Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn			
130	135	140	
Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly			
145	150	155	160
Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu			
165	170	175	
Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His			
180	185	190	
Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met			
195	200	205	
Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp			
210	215	220	
Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu			
225	230	235	240
Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala			

245 250 255  
Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His Trp Lys Gly Asn  
260 265 270  
Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys Phe Ser Leu Glu  
275 280 285  
Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu Gly Met Thr Asp  
290 295 300  
Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu  
305 310 315 320  
Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn  
325 330 335  
Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala  
340 345 350  
Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val  
355 360 365  
Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met  
370 375 380  
Glu Pro  
385

&lt;210&gt; 89

&lt;211&gt; 1412

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (52).. (1341)

&lt;400&gt; 89

cggggtcgtc cgcaaagcct gagicctgtc ctftctctct ccccgacag c atg agc 57

Met Ser

1

ttc acc act cgc tcc acc ttc tcc acc aac tac cgg tcc ctg ggc tct 105

Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu Gly Ser

5

10

15

gtc cag gcg ccc agc tac ggc gcc cgg ccg gtc agc agc gcg gcc agc 153

Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala Ala Ser

20

25

30

gtc tat gca ggc gct ggg ggc tct ggt tcc cgg atc tcc gtg tcc cgc 201

Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val Ser Arg

35

40

45

50

tcc acc agc ttc agg ggc ggc atg ggg tcc ggg ggc ctg gcc acc ggg 249

Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr Gly

55

60

65

ata gcc ggg ggt ctg gca gga atg gga ggc atc cag aac gag aag gag 297

Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys Glu

70

75

80

acc atg caa agc ctg aac gac cgc ctg gcc tct tac ctg gac aga gtg 345

Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg Val

85

90

95

agg agc ctg gag acc gag aac cgg agg ctg gag agc aaa atc cgg gag 393

Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg Glu

100

105

110

cac ttg gag aag aag gga ccc cag gtc aga gac tgg agc cat tac ttc 441

His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr Phe

115	120	125	130	
aag atc atc gag gac ctg agg gct cag atc ttc gca aat act gtg gac	489			
Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val Asp				
	135	140	145	
aat gcc cgc atc gtt ctg cag att gac aat gcc cgt ctt gct gct gat	537			
Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala Asp				
	150	155	160	
gac ttt aga gtc aag tat gag aca gag ctg gcc atg cgc cag tct gtg	585			
Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser Val				
	165	170	175	
gag aac gac atc cat ggg ctc cgc aag gtc att gat gac acc aat atc	633			
Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn Ile				
	180	185	190	
aca cga ctg cag ctg gag aca gag atc gag gct ctc aag gag gag ctg	681			
Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu Leu				
	195	200	205	210
ctc ttc atg aag aag aac cac gaa gag gaa gta aaa ggc cta caa gcc	729			
Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln Ala				
	215	220	225	
cag att gcc agc tct ggg ttg acc gtg gag gta gat gcc ccc aaa tct	777			
Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys Ser				
	230	235	240	
cag gac ctc gcc aag atc atg gca gac atc cgg gcc caa tat gac gag	825			
Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp Glu				
	245	250	255	
ctg gct cgg aag aac cga gag gag cta gac aag tac tgg tct cag cag	873			

Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln Gln  
 260 265 270  
 att gag gag agc acc aca gtg gtc acc aca cag tct gct gag gtt gga 921  
 Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val Gly  
 275 280 285 290  
 gct gct gag acg acg ctc aca gag ctg aga cgt aca gtc cag tcc ttg 969  
 Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser Leu  
 295 300 305  
 gag atc gac ctg gac tcc atg aga aat ctg aag gcc agc ttg gag aac 1017  
 Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu Asn  
 310 315 320  
 agc ctg agg gag gtg gag gcc cgc tac gcc cta cag atg gag cag ctc 1065  
 Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln Leu  
 325 330 335  
 aac ggg atc ctg ctg cac ctt gag tca gag ctg gca cag acc cgg gca 1113  
 Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg Ala  
 340 345 350  
 gag gga cag cgc cag gcc cag gag tat gag gcc ctg ctg aac atc aag 1161  
 Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile Lys  
 355 360 365 370  
 gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa gat 1209  
 Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Asp  
 375 380 385  
 ggc gag gac ttt aat ctt ggt gat gcc ttg gac agc agc aac tcc atg 1257  
 Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser Met  
 390 395 400  
 caa acc atc caa aag acc acc acc cgc cgg ata gtg gat ggc aaa gtg 1305

Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys Val

405

410

415

gtg tct gag acc aat gac acc aaa gtt ctg agg cat taagccagca 1351

Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His

420

425

430

gaagcagggt accctttggg gagcaggagg ccaataaaaa gttcagagtt cattggatgt 1411

c 1412

<210> 90

<211> 430

<212> PRT

<213> Homo sapiens

<400> 90

Met Ser Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu

1

5

10

15

Gly Ser Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala

20

25

30

Ala Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val

35

40

45

Ser Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala

50

55

60

Thr Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu

65

70

75

80

Lys Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp

85

90

95

Arg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile

100

105

110

Arg Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His  
115 120 125  
Tyr Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr  
130 135 140  
Val Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala  
145 150 155 160  
Ala Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln  
165 170 175  
Ser Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr  
180 185 190  
Asn Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu  
195 200 205  
Glu Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu  
210 215 220  
Gln Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro  
225 230 235 240  
Lys Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr  
245 250 255  
Asp Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser  
260 265 270  
Gln Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu  
275 280 285  
Val Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln  
290 295 300  
Ser Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu  
305 310 315 320



Glu Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu

325

330

335

Gln Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr

340

345

350

Arg Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn

355

360

365

Ile Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu

370

375

380

Glu Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn

385

390

395

400

Ser Met Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly

405

410

415

Lys Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His

420

425

430

<210> 91

<211> 1040

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (171).. (968)

<400> 91

gggcagacga tgctgaagat gctctccitt aagctgctgc tgctggccgt ggctctgggc 60

tctcttgaag gagatgctaa gtttggggaa agaaacgaag ggagcggaca aggaggagaa 120

ggtgccctgaa tgggaacccc ccgaagcgcc tgaaaaggag agacaggagg atg atg 176

Met Met

1

tcc cag ctg gag ctg ctg agt ggg gga gag atg ctg tgc ggt ggc ttc 224  
 Ser Gln Leu Glu Leu Leu Ser Gly Gly Glu Met Leu Cys Gly Gly Phe  
           5                  10                  15  
 tac cct cgg ctg tcc tgc tgc ctg cgg agt gac agc ccg ggg cta ggg 272  
 Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly Leu Gly  
           20                  25                  30  
 cgc ctg gag aat aag ata ttt tct gtt acc aac aac aca gaa tgt ggg 320  
 Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu Cys Gly  
           35                  40                  45                  50  
 aag tta ctg gag gaa atc aaa tgt gca ctt tgc tct cca cat tct caa 368  
 Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His Ser Gln  
                   55                  60                  65  
 agc ctg ttc cac tca cct gag aga gaa gtc ttg gaa aga gac cta gta 416  
 Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp Leu Val  
           70                  75                  80  
 ctt cct ctg ctc tgc aaa gac tat tgc aaa gaa ttc tti tac act tgc 464  
 Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr Thr Cys  
           85                  90                  95  
 cga ggc cat att cca ggt ttc ctt caa aca act gcg gat gag ttt tgc 512  
 Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu Phe Cys  
           100                  105                  110  
 ttt tac tat gca aga aaa gat ggt ggg ttg tgc ttt cca gat ttt cca 560  
 Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp Phe Pro  
           115                  120                  125                  130  
 aga aaa caa gtc aga gga cca gca tct aac tac ttg gac cag atg gaa 608  
 Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln Met Glu

135	140	145	
gaa tat gac aaa gtg gaa gag atc agc aga aag cac aaa cac aac tgc			656
Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His Asn Cys			
150	155	160	
ttc tgt att cag gag gtt gtg agt ggg ctg cgg cag ccc gtt ggt gcc			704
Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val Gly Ala			
165	170	175	
ctg cat agt ggg gat ggc tgc caa cgt ctc ttc att ctg gaa aaa gaa			752
Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu Lys Glu			
180	185	190	
ggt tat gtg aag ata ctt acc cct gaa gga gaa att ttc aag gag cct			800
Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro			
195	200	205	210
tat ttg gac att cac aaa ctt gtt caa agt gga ata aag gtt ggc ttt			848
Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val Gly Phe			
215	220	225	
tta aat ttt att tat ttt tgt gct ggc tac gtt aat ttt att tta gtg			896
Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile Leu Val			
230	235	240	
tta cct tcc tca ctg aag gta ttt ctt tgt aat aaa aga aag aat ctt			944
Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys Asn Leu			
245	250	255	
gca gga gaa aat aag ggg gca aca taagaaacaa taattatggc acctgaatta			998
Ala Gly Glu Asn Lys Gly Ala Thr			
260	265		
ggacagtgc attaaakgtt ggctktttaw attttaaaaa aa			1040

&lt;210&gt; 92

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

Met Met Ser Gln Leu Glu Leu Leu Ser Gly Gly Glu Met Leu Cys Gly

1 5 10 15

Gly Phe Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly

20 25 30

Leu Gly Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu

35 40 45

Cys Gly Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His

50 55 60

Ser Gln Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp

65 70 75 80

Leu Val Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr

85 90 95

Thr Cys Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu

100 105 110

Phe Cys Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp

115 120 125

Phe Pro Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln

130 135 140

Met Glu Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His

145 150 155 160

Asn Cys Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val

165 170 175  
 Gly Ala Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu  
 180 185 190  
 Lys Glu Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys  
 195 200 205  
 Glu Pro Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val  
 210 215 220  
 Gly Phe Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile  
 225 230 235 240  
 Leu Val Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys  
 245 250 255  
 Asn Leu Ala Gly Glu Asn Lys Gly Ala Thr  
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<210> 93

<211> 1639

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75).. (371)

<400> 93

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 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala  
 1 5 10  
 ttc ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt 158

Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser  
           15                    20                    25  
 gct aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc 206  
 Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe  
           30                    35                    40  
 cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac 254  
 His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His  
           45                    50                    55                    60  
 tgc gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc 302  
 Cys Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu  
                                 65                    70                    75  
 tgt ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt 350  
 Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe  
                                 80                    85                    90  
 ttg aag agg gct gag aat tca taaaaaatt cattctctgt ggtatccaag 401  
 Leu Lys Arg Ala Glu Asn Ser  
                                 95  
 aatcagtga gatgccagt aaacttcaag caaatctact tcaacacttc atgtattgtg 461  
 tgggtctgtt gtagggttgc cagatgcaat acaagattcc tggttaaatt tgaatttcag 521  
 taaacaatga atagtttttc attgtaccat gaaatatcca gaacatactt atatgtaaag 581  
 tattatttat ttgaatctac aaaaaacaac aaataatttt taaatataag gattttccta 641  
 gatattgcac gggagaatat acaaatagca aaattgagcc aaggccaag agaatatccg 701  
 aactttaatt tcaggaattg aatgggttg ctagaatgtg atatttgaag catcacataa 761  
 aaatgatggg acaataaatt ttgccataaa gtcaaattta gctggaaatc ctggattttt 821  
 ttctgtttaa tctggcaacc ctagtctgct agccaggatc cacaagtcct tgttccactg 881  
 tgccttgggt tctccittat ttctaagtgg aaaaagtatt agccaccatc ttacctcaca 941  
 gtagtgttgt gaggacatgt ggaagcactt taagtfffft catcataaca taaattattt 1001

tcaagigtaa cttattaacc tatattat tatatgtatt atttaagcat caaatatttg 1061  
 tgcaagaatt lggaaaaata gaagatgaat catigattga atagtataa agatgtata 1121  
 gtaaatllat tttattttag atattaaatg atgttttatt agataaatll caatcagggt 1181  
 tttlagatta aacaaagaaa caatlgggta cccagttaaa tttcatllc agataaaca 1241  
 caaataattt tttagtataa gtacattatt gttatctga aagttttaat tgaactaaca 1301  
 atccatgttt gatactccca gctctgcat tgcagctgt gttggtagtg ctgtgttgaa 1361  
 ttacggaata atgagttaga actattaaaa cagccaaaac tccacagica atattagtaa 1421  
 tttcttgctg gttgaaactt gttattatg tacaaataga ttcttataat attattttaa 1481  
 tgactgcatt tttaaalaca aggttttata tttttaactt taagatgttt ttatgtgctc 1541  
 tccaaatttt ttttactgtt tctgattgta tggaaatata aaagtaaata tgaacattt 1601  
 aaaatataat ttgttgtcaa aglaaaaaaa aaaaaaaa 1639

<210> 94

<211> 99

<212> PRT

<213> Homo sapiens

<400> 94

Met	Thr	Ser	Lys	Leu	Ala	Val	Ala	Leu	Leu	Ala	Ala	Phe	Leu	Ile	Ser
Ala	Ala	Leu	Cys	Glu	Gly	Ala	Val	Leu	Pro	Arg	Ser	Ala	Lys	Glu	Leu
1				5					10					15	
Arg	Cys	Gln	Cys	Ile	Lys	Thr	Tyr	Ser	Lys	Pro	Phe	His	Pro	Lys	Phe
				20					25					30	
Ile	Lys	Glu	Leu	Arg	Val	Ile	Glu	Ser	Gly	Pro	His	Cys	Ala	Asn	Thr
				35					40					45	
Glu	Ile	Ile	Val	Lys	Leu	Ser	Asp	Gly	Arg	Glu	Leu	Cys	Leu	Asp	Pro
				50					55					60	
Lys	Glu	Asn	Trp	Val	Gln	Arg	Val	Val	Glu	Lys	Phe	Leu	Lys	Arg	Ala

65                      70                      75                      80

Glu Asn Ser

<210> 95

<211> 3293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (8).. (1945)

<400> 95

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tgc tgc tgc tgt cct cgc gtc gcg ggt gtg ccc gga gag gct gag cag 97
Cys Cys Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln
      15              20              25              30
cct gcg cct gag ctg gtg gag gtg gaa gtg ggc agc aca gcc ctt ctg 145
Pro Ala Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu
          35              40              45
aag tgc ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg 193
Lys Cys Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp
          50              55              60
ttt tct gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag 241
Phe Ser Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln
          65              70              75
ggc cag ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc 289

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Gly Gln Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu  
 80 85 90  
 cag gac aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac 337  
 Gln Asp Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp  
 95 100 105 110  
 gag cgc atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac 385  
 Glu Arg Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr  
 115 120 125  
 cgc atc cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag 433  
 Arg Ile Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln  
 130 135 140  
 gtc aac ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc 481  
 Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val  
 145 150 155  
 gct acc tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg 529  
 Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp  
 160 165 170  
 tac aag aat ggc cgg cct ctg aag gag gag aag aac cgg gtc cac att 577  
 Tyr Lys Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile  
 175 180 185 190  
 cag tcg tcc cag act gtg gag tcg agt ggt ttg tac acc ttg cag agt 625  
 Gln Ser Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser  
 195 200 205  
 att ctg aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac 673  
 Ile Leu Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr  
 210 215 220

tgt gag ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc 721  
 Cys Glu Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser  
 225 230 235  
 agg gaa gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtg tgg ctg 769  
 Arg Glu Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu  
 240 245 250  
 gaa gtg gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc 817  
 Glu Val Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile  
 255 260 265 270  
 agg tgt ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag 865  
 Arg Cys Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys  
 275 280 285  
 cag aac ccc agc acc agg gag gca gag gaa gag aca acc aac gac aac 913  
 Gln Asn Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn  
 290 295 300  
 ggg gtc ctg gtg ctg gag cct gcc cgg aag gaa cac agt ggg cgc tat 961  
 Gly Val Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr  
 305 310 315  
 gaa tgt cag gcc tgg aac ttg gac acc atg ata tcg ctg ctg agt gaa 1009  
 Glu Cys Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu  
 320 325 330  
 cca cag gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc 1057  
 Pro Gln Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro  
 335 340 345 350  
 gca gcc cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag 1105  
 Ala Ala Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu  
 355 360 365

gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca 1153  
 Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr  
 370 375 380  
 gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa 1201  
 Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys  
 385 390 395  
 cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata 1249  
 Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile  
 400 405 410  
 ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc 1297  
 Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro  
 415 420 425 430  
 cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg 1345  
 Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met  
 435 440 445  
 gtg tlg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc 1393  
 Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile  
 450 455 460  
 tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag 1441  
 Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln  
 465 470 475  
 cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag 1489  
 Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu  
 480 485 490  
 aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc 1537  
 Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser

495                      500                      505                      510  
 atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc 1585  
 Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser  
                     515                      520                      525  
 aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga 1633  
 Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg  
                     530                      535                      540  
 gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg 1681  
 Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg  
                     545                      550                      555  
 ggc gtg gtc atc glg gct gtg att glg tgc atc ctg gtc ctg gcg gtg 1729  
 Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val  
                     560                      565                      570  
 ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc 1777  
 Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys  
 575                      580                      585                      590  
 agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc 1825  
 Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr  
                     595                      600                      605  
 gaa ctt gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc 1873  
 Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly  
                     610                      615                      620  
 ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga 1921  
 Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly  
                     625                      630                      635  
 gag aaa tac atc gat ctg agg cat tagccccgaa tcacttcagc tcccttcct 1975  
 Glu Lys Tyr Ile Asp Leu Arg His

640

645

gccigggacca ttcccagctc ccigctcact ctctctcag ccaaagctca aagggactag 2035  
 agagaagcct ccigctcccc tcgctgcac acccccttc agagggccac tgggttagga 2095  
 cctgaggacc tcacttggcc ctgcaaggcc cgcttttcag ggaccagtcc accaccatct 2155  
 cciccacgtt gaglgaagct catccaagc aaggagcccc agctctccga gcgggiagga 2215  
 gagtttcttg cagaacgtgt ttttcttta cacacattat gctgtaaata cgctcgtcct 2275  
 gccagcagct gagctgggta gcctctctga gctggtttcc tgcccaaaag gctggcattc 2335  
 caccatccag gtcaccact gaagtgagga cacaccggag ccaggcgccct gctcatgttg 2395  
 aagtgcgtcg ttcacacccg ctccggagag caccacagca gcatccagaa gcagctgcag 2455  
 tgcaagcttg catgcctgcg tgttgcctga ccacctcct gctgcctct tcaaagtctc 2515  
 ctgtgacatt tttcttttgg tcagaggcca ggaacttgtt catctcttaa agatcgtgc 2575  
 cggggccagg tgtggctcac gcctglaac ccagcacitt gggaggccga ggcggcggat 2635  
 cacaagctca gacgagacca tcctggctaa cacggtgaaa cctgtctct actaaaaata 2695  
 caaaaaaaaa tttagctaggc gtagtgggtg gcacctatag tcccagctac tcggaaggct 2755  
 gaagcaggag aatggatga atccaggagg tggagcttgc agtgagccga gaccgtgcca 2815  
 ctgcactcca gcctgggcaa cacagcgaga ctccgtctcg aggaaaaaaaaa aaatcgtgct 2875  
 cgtagcagct ggctctgttt cgagtcaggt gaattagcct caatccccgt gttcacttgc 2935  
 tcccatagcc ctcttgatgg atcacglaaa actgaaaggc agcggggagc agacaaagat 2995  
 gaggtctaca ctgtccttca tggggattaa agctatggtt atattagcac caaacitcta 3055  
 caaaccaagc tcaggacca accctagaag ggcccaaatg agagaatggt acttagggat 3115  
 ggcaaaacgg gcctggctag agcttcgggt gtgtgtgtgt gtcigtgtat gcatacatat 3175  
 gtgtgtatat atggttttgt caggltgtga aatttgcaa ttgtttcctt tatatatgta 3235  
 tgtatatata tatatgaaaa tatatatata tatgaaaaat aaagcttaat tgtcccag 3293

&lt;210&gt; 96

&lt;211&gt; 646

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala Cys Cys

1 5 10 15

Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala

20 25 30

Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys

35 40 45

Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser

50 55 60

Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln

65 70 75 80

Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp

85 90 95

Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg

100 105 110

Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile

115 120 125

Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn

130 135 140

Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr

145 150 155 160

Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys

165 170 175

Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser

180 185 190

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Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu  
 195 200 205  
 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu  
 210 215 220  
 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu  
 225 230 235 240  
 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val  
 245 250 255  
 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys  
 260 265 270  
 Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn  
 275 280 285  
 Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val  
 290 295 300  
 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys  
 305 310 315 320  
 Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln  
 325 330 335  
 Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala  
 340 345 350  
 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu  
 355 360 365  
 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln  
 370 375 380  
 Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu  
 385 390 395 400  
 Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly

405 410 415  
 Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp  
 420 425 430  
 Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu  
 435 440 445  
 Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp  
 450 455 460  
 Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val  
 465 470 475 480  
 Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly  
 485 490 495  
 Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu  
 500 505 510  
 Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr  
 515 520 525  
 Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn  
 530 535 540  
 Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val  
 545 550 555 560  
 Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly  
 565 570 575  
 Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg  
 580 585 590  
 Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu  
 595 600 605  
 Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu



610                      615                      620  
 Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys  
 625                      630                      635                      640  
 Tyr Ile Asp Leu Arg His  
                          645

<210> 97

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (158).. (1279)

<400> 97

gaatcggcgg tcccgaggt cccgcatgtt gcggacagta tgaggcaagc gcagggggac 60  
 ggggaccagc agctgtcgcc gccgcctcga gggagaagag ggaacagaaa tctttgcccc 120  
 ctgactttgg aaatctcggt taaccttcaa actggcg atg tca agg gtt cca agt 175

Met Ser Arg Val Pro Ser

1

5

cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223

Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp

10

15

20

tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271

Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile

25

30

35

aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319

Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser

40	45	50	
tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga	367		
Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg			
55	60	65	70
gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt	415		
Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu			
75	80	85	
tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cgg gca aaa ttc	463		
Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe			
90	95	100	
aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag	511		
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu			
105	110	115	
agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag	559		
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys			
120	125	130	
aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc	607		
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu			
135	140	145	150
cct gat gac aag ctt acc ctc ttc tgc gag glg agt gtt gtg caa gat	655		
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp			
155	160	165	
tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct	703		
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro			
170	175	180	
gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg	751		
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg			

185	190	195	
ttc aca gac tgc tgc ttg tgt gtt gcc ggc cag gaa ttc cag gct cac	799		
Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His			
200	205	210	
aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa	847		
Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu			
215	220	225	230
cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg	895		
His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val			
235	240	245	
gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag	943		
Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys			
250	255	260	
gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac	991		
Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp			
265	270	275	
aag tat gcc ctg gag cgc tta aag gtc atg tgt gag gat gcc ctc tgc	1039		
Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys			
280	285	290	
agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac	1087		
Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp			
295	300	305	310
ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac	1135		
Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn			
315	320	325	
tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg	1183		

Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val  
                   330                  335                  340  
 gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca 1231  
 Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser  
                   345                  350                  355  
 gca cag tgc cct ttt ctg gga ccc cca cgc aaa cgc ctg aag caa tcc 1279  
 Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser  
                   360                  365                  370  
 taagatcctg ctgttgttaa gactccgttt aattccaga agcagcagcc acgtttgctg 1339  
 ccacigacca ccaggtagac agcgcaatct gaggagcttt tactctgttg tgagggaag 1399  
 agactgcatt gggcccccag acttttaaaa cagcactaaa taacttgagg gaaacggggg 1459  
 gagggaaaat gaaatgaaaa cctgttgct gcgtcactgt gtccctttg gcctgtctga 1519  
 gtttgatact gtggggattc agtttaggcg ctggcccgag gataccag cggtggtact 1579  
 tcggagacac ctgtctgcat ctgactgagc agaacaatc gtcaggigcc tggagcaaaa 1639  
 agg 1642

&lt;210&gt; 98

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

Met Ser Arg Val Pro Ser Pro Pro Pro Pro Ala Glu Met Ser Ser Gly  
           1                  5                  10                  15  
 Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe  
                   20                  25                  30  
 Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met  
                   35                  40                  45

Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys  
 50 55 60  
 Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser  
 65 70 75 80  
 Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser  
 85 90 95  
 Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu  
 100 105 110  
 Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly  
 115 120 125  
 Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp  
 130 135 140  
 Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu  
 145 150 155 160  
 Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met  
 165 170 175  
 Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly  
 180 185 190  
 Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly  
 195 200 205  
 Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val  
 210 215 220  
 Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg  
 225 230 235 240  
 Val Glu Ile Asn Asp Val Glu Pro Glu Val Phe Lys Glu Met Met Cys  
 245 250 255  
 Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp

260 265 270  
 Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met  
 275 280 285  
 Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu  
 290 295 300  
 Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln  
 305 310 315 320  
 Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser  
 325 330 335  
 Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala  
 340 345 350  
 Tyr Arg Ser Leu Ala Ser Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg  
 355 360 365  
 Lys Arg Leu Lys Gln Ser  
 370

&lt;210&gt; 99

&lt;211&gt; 5722

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (112).. (3621)

&lt;400&gt; 99

ggacgcacag gcatlccccg cgccccctcca gccctcgccg ccctcgccac cgctcccggc 60  
 cgccgcgctc cggtacacac aggatccctg ctgggcacca acagctccac c atg ggg 117

Met Gly

1

ctg gcc tgg gga cta ggc gtc ctg ttc ctg atg cat gtg tgt ggc acc 165  
 Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr  
                   5                  10                  15  
 aac cgc att cca gag tct ggc gga gac aac agc gtg ttt gac atc ttt 213  
 Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp Ile Phe  
                   20                  25                  30  
 gaa ctc acc ggg gcc gcc cgc aag ggg tct ggg cgc cga ctg gtg aag 261  
 Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu Val Lys  
                   35                  40                  45                  50  
 ggc ccc gac cct tcc agc cca gct ttc cgc atc gag gat gcc aac ctg 309  
 Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala Asn Leu  
                   55                  60                  65  
 atc ccc cct gtg cct gat gac aag ttc caa gac ctg gtg gat gct gtg 357  
 Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp Ala Val  
                   70                  75                  80  
 cgg gca gaa aag ggt ttc ctc ctt ctg gca tcc ctg agg cag atg aag 405  
 Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln Met Lys  
                   85                  90                  95  
 aag acc cgg ggc acg ctg ctg gcc ctg gag cgg aaa gac cac tct ggc 453  
 Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His Ser Gly  
                   100                  105                  110  
 cag gtc ttc agc gtg gtg tcc aat ggc aag gcg ggc acc ctg gac ctc 501  
 Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu Asp Leu  
                   115                  120                  125                  130  
 agc ctg acc gtc caa gga aag cag cac gtg gtg tct gtg gaa gaa gct 549

Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu Glu Ala  
 135 140 145  
 ctc ctg gca acc ggc cag tgg aag agc atc acc ctg ttt gtc cag gaa 597  
 Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val Gln Glu  
 150 155 160  
 gac agg gcc cag ctg tac atc gac tgt gaa aag atg gag aat gct gag 645  
 Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn Ala Glu  
 165 170 175  
 ttg gac gtc ccc atc caa agc gtc ttc acc aga gac ctg gcc agc atc 693  
 Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala Ser Ile  
 180 185 190  
 gcc aga ctc cgc atc gca aag ggg ggc gtc aat gac aat ttc cag ggg 741  
 Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe Gln Gly  
 195 200 205 210  
 gtg ctg cag aat gtg agg ttt gtc ttt gga acc aca cca gaa gac atc 789  
 Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu Asp Ile  
 215 220 225  
 ctc agg aac aaa ggc tgc tcc agc tct acc agt gtc ctc ctc acc ctt 837  
 Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu Thr Leu  
 230 235 240  
 gac aac aac gtg gtg aat ggt tcc agc cct gcc atc cgc act aac tac 885  
 Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr Asn Tyr  
 245 250 255  
 att ggc cac aag aca aag gac ttg caa gcc atc tgc ggc atc tcc tgt 933  
 Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile Ser Cys  
 260 265 270  
 gat gag ctg tcc agc atg gtc ctg gaa ctc agg ggc ctg cgc acc att 981



Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg Thr Ile  
 275 280 285 290  
 gtg acc acg ctg cag gac agc atc cgc aaa gtg act gaa gag aac aaa 1029  
 Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu Asn Lys  
 295 300 305  
 gag ttg gcc aat gag ctg agg cgg cct ccc cta tgc tat cac aac gga 1077  
 Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly  
 310 315 320  
 gtt cag tac aga aat aac gag gaa tgg act gtt gat agc tgc act gag 1125  
 Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys Thr Glu  
 325 330 335  
 tgt cac tgt cag aac tca gtt acc atc tgc aaa aag gtg tcc tgc ccc 1173  
 Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser Cys Pro  
 340 345 350  
 atc atg ccc tgc tcc aat gcc aca gtt cct gat gga gaa tgc tgt cct 1221  
 Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys Cys Pro  
 355 360 365 370  
 cgc tgt tgg ccc agc gac tct gcg gac gat ggc tgg tct cca tgg tcc 1269  
 Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro Trp Ser  
 375 380 385  
 gag tgg acc tcc tgt tct acg agc tgt ggc aat gga att cag cag cgc 1317  
 Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln Gln Arg  
 390 395 400  
 ggc cgc tcc tgc gat agc ctc aac aac cga tgt gag ggc tcc tgc gtc 1365  
 Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser Ser Val  
 405 410 415

cag aca cgg acc tgc cac att cag gag tgt gac aaa aga ttt aaa cag 1413  
 Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe Lys Gln  
 420 425 430  
 gat ggt ggc tgg agc cac tgg tcc ccg tgg tca tct tgt tct gtg aca 1461  
 Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr  
 435 440 445 450  
 tgt ggt gat ggt gtg atc aca agg atc cgg ctc tgc aac tct ccc agc 1509  
 Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser  
 455 460 465  
 ccc cag atg aat ggg aaa ccc tgt gaa ggc gaa gcg cgg gag acc aaa 1557  
 Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys  
 470 475 480  
 gcc tgc aag aaa gac gcc tgc ccc atc aat gga ggc tgg ggt cct tgg 1605  
 Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly Pro Trp  
 485 490 495  
 tca cca tgg gac atc tgt tct gtc acc tgt gga gga ggg gta cag aaa 1653  
 Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val Gln Lys  
 500 505 510  
 cgt agt cgt ctc tgc aac aac ccc gca ccc cag ttt gga ggc aag gac 1701  
 Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly Lys Asp  
 515 520 525 530  
 tgc gtt ggt gat gta aca gaa aac cag atc tgc aac aag cag gac tgt 1749  
 Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys  
 535 540 545  
 cca att gat gga tgc ctg tcc aat ccc tgc ttt gcc ggc gtg aag tgt 1797  
 Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys  
 550 555 560

WO 01/25427

act agc tac cct gat ggc agc tgg aaa tgt ggt gct tgt ccc cct ggt 1845  
 Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro Pro Gly  
 565 570 575  
 tac agt gga aat ggc atc cag tgc aca gat gtt gat gag tgc aaa gaa 1893  
 Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys Lys Glu  
 580 585 590  
 gtg cct gat gcc tgc ttc aac cac aat gga gag cac cgg tgt gag aac 1941  
 Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys Glu Asn  
 595 600 605 610  
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 Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe Thr Gly  
 615 620 625  
 tca cag ccc ttc ggc cag ggt gtc gaa cat gcc acg gcc aac aaa cag 2037  
 Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn Lys Gln  
 630 635 640  
 gtg tgc aag ccc cgt aac ccc tgc acg gat ggg acc cac gac tgc aac 2085  
 Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn  
 645 650 655  
 aag aac gcc aag tgc aac tac ctg ggc cac tat agc gac ccc atg tac 2133  
 Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr  
 660 665 670  
 cgc tgc gag tgc aag cct ggc tac gct ggc aat ggc atc atc tgc ggg 2181  
 Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly  
 675 680 685 690  
 gag gac aca gac ctg gat ggc tgg ccc aat gag aac ctg gtg tgc gtg 2229  
 Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val

695	700	705	
gcc aat gcg act tac cac tgc aaa aag gat aat tgc ccc aac ctt ccc	2277		
Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro			
710	715	720	
aac tca ggg cag gaa gac tat gac aag gat gga att ggt gat gcc tgt	2325		
Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys			
725	730	735	
gat gat gac gat gac aat gat aaa att cca gat gac agg gac aac tgt	2373		
Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys			
740	745	750	
cca ttc cat tac aac cca gct cag tat gac tat gac aga gat gat gtg	2421		
Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val			
755	760	765	770
gga gac cgc tgt gac aac tgt ccc tac aac cac aac cca gat cag gca	2469		
Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala			
775	780	785	
gac aca gac aac aat ggg gaa gga gac gcc tgt gct gca gac att gat	2517		
Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp			
790	795	800	
gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat	2565		
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn			
805	810	815	
gtg gac cag aga gac act gat atg gat ggg gtt gga gat cag tgt gac	2613		
Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp			
820	825	830	
aat tgc ccc ttg gaa cac aat ccg gat cag ctg gac tct gac tca gac	2661		
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp			

835	840	845	850	
cgc att gga gat acc tgt gac aac aat cag gai att gat gaa gat ggc	2709			
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly				
855	860	865		
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag	2757			
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln				
870	875	880		
gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat	2805			
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp				
885	890	895		
gac aac gat ggc att cct gat gac aag gac aac tgc aga ctc gtg ccc	2853			
Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro				
900	905	910		
aat ccc gac cag aag gac tct gac ggc gat ggt cga ggt gat gcc tgc	2901			
Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys				
915	920	925	930	
aaa gat gat ttt gac cat gac agt gtg cca gac atc gat gac atc tgt	2949			
Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys				
935	940	945		
cct gag aat gtt gac atc agt gag acc gat ttc cgc cga ttc cag atg	2997			
Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met				
950	955	960		
att cct ctg gac ccc aaa ggg aca tcc caa aat gac cct aac tgg gtt	3045			
Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val				
965	970	975		
gta cgc cat cag ggt aaa gaa ctc gtc cag act gtc aac tgt gat cct	3093			

Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro  
 980 985 990  
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 Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe Ser Gly  
 995 1000 1005 1010  
 acc ttc ttc atc aac acc gaa agg gac gat gac tat gct gga ttt gtc 3189  
 Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly Phe Val  
 1015 1020 1025  
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 Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln  
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 gtc acc cag tcc tac tgg gac acc aac ccc acg agg gct cag gga tac 3285  
 Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln Gly Tyr  
 1045 1050 1055  
 tcg ggc ctt tct gtg aaa gtt gta aac tcc acc aca ggc cct ggc gag 3333  
 Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro Gly Glu  
 1060 1065 1070  
 cac ctg cgg aac gcc ctg tgg cac aca gga aac acc cct ggc cag gtg 3381  
 His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val  
 1075 1080 1085 1090  
 cgc acc ctg tgg cat gac cct cgt cac ata ggc tgg aaa gat ttc acc 3429  
 Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp Phe Thr  
 1095 1100 1105  
 gcc tac aga tgg cgt ctc agc cac agg cca aag acg ggt ttc att aga 3477  
 Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg  
 1110 1115 1120  
 gtg gtg atg tat gaa ggg aag aaa atc atg gct gac tca gga ccc atc 3525

Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile

1125

1130

1135

tat gat aaa acc tat gct ggt ggt aga cta ggg ttg ttt gtc ttc tct 3573

Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser

1140

1145

1150

caa gaa atg gtg ttc ttc tct gac ctg aaa tac gaa tgt aga gat ccc 3621

Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Pro

1155

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1165

1170

taatcatcaa attgttgatt gaaagactga tcataaacca atgctggtat tgcaccttct 3681

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ttgcitttgt ttccttttga aaaagcatct acttgcttca gtgggaagg tgcccatctc 3921

actctgcctt tgtcacagag cagggtgcta ttgtgaggcc atctctgagc agtggactca 3981

aaagcatitt caggcatgtc agagaaggga ggactcacia gaattagcaa acaaaaccac 4041

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taaccaatgt aaataggcac tlaaatagaa gcaggaaagg gagacaaaga ctggcttctg 4281

gacttctctc ctgatcccca cctttactca tcaccttgca gtggccagaa ttagggaatc 4341

agaatcaaac cagtgttaagg cagtgcctggc tgccattgcc tggtcacatt gaaattggig 4401

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tggcacaaaa ttattatcaa cctaactaaa acattccttt tctctttttt ccgtaattac 4581

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aaatatttat tttttactta ttciggaaga tctggcigaa ggattattca tggaacagga 4701

agaagcgtaa agactatcca tgtcatcttt gttagagagtc ttcgtagctg taagattgta 4761  
 aalacagatt aattatlaac tctgttcctgc ctggaaattt aggcctcata cggaaaggtg 4821  
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 cagctlaata agctgcctgc ccccttgctc tcagagtgga tgtaatggga ttcccttttt 4941  
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 gagaaggaaa gcatatacac tttttctttt catttttcca aaagagaaaa aaatgacaaa 5121  
 aggtgaaact tacatacaaa tattacctca ttgttttgtg gactgagtaa agaatttttg 5181  
 gatcaagcgg aaagagttaa agtgtctaac aaacttaaag ctactgtagt acctaaaaag 5241  
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 tgaaatgta aatacaattt ctgaaagta tgtttttttt ctatcatctg gtataccatt 5361  
 gctttatatt tataaattat ttctcatctg ccattggaat agaataitca gattgtgtag 5421  
 atatgctatt taaataattt atcaggaaat actgcctgta gagttagtat ttctattttt 5481  
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 taggaatgtg cttttttttg tacacatttt tatccatttt acattctaaa gcagtgtaag 5661  
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<210> 100

<211> 1170

<212> PRT

<213> Homo sapiens

<400> 100

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys

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Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp



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20 25 30  
 Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu  
 35 40 45  
 Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala  
 50 55 60  
 Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp  
 65 70 75 80  
 Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln  
 85 90 95  
 Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His  
 100 105 110  
 Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu  
 115 120 125  
 Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu  
 130 135 140  
 Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val  
 145 150 155 160  
 Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn  
 165 170 175  
 Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala  
 180 185 190  
 Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe  
 195 200 205  
 Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu  
 210 215 220  
 Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu  
 225 230 235 240

WO 01/25427

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr  
 245 250 255  
 Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile  
 260 265 270  
 Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg  
 275 280 285  
 Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu  
 290 295 300  
 Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His  
 305 310 315 320  
 Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys  
 325 330 335  
 Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser  
 340 345 350  
 Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys  
 355 360 365  
 Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro  
 370 375 380  
 Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln  
 385 390 395 400  
 Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser  
 405 410 415  
 Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe  
 420 425 430  
 Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser  
 435 440 445

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser  
450 455 460  
Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu  
465 470 475 480  
Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly  
485 490 495  
Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val  
500 505 510  
Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly  
515 520 525  
Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln  
530 535 540  
Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val  
545 550 555 560  
Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro  
565 570 575  
Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys  
580 585 590  
Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys  
595 600 605  
Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe  
610 615 620  
Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn  
625 630 635 640  
Lys Gln Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp  
645 650 655  
Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro

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660	665	670	
Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile			
675	680	685	
Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val			
690	695	700	
Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn			
705	710	715	720
Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp			
725	730	735	
Ala Cys Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp			
740	745	750	
Asn Cys Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp			
755	760	765	
Asp Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp			
770	775	780	
Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp			
785	790	795	800
Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val			
805	810	815	
Tyr Asn Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln			
820	825	830	
Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp			
835	840	845	
Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu			
850	855	860	
Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala			

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865                      870                      875                      880  
 Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His  
                          885                      890                      895  
 Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu  
                          900                      905                      910  
 Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp  
                          915                      920                      925  
 Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp  
                          930                      935                      940  
 Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe  
 945                      950                      955                      960  
 Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn  
                          965                      970                      975  
 Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys  
                          980                      985                      990  
 Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe  
                          995                      1000                      1005  
 Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly  
                          1010                      1015                      1020  
 Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp  
 1025                      1030                      1035                      1040  
 Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln  
                          1045                      1050                      1055  
 Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro  
                          1060                      1065                      1070  
 Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly  
                          1075                      1080                      1085

Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp

1090

1095

1100

Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe

1105

1110

1115

1120

Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly

1125

1130

1135

Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val

1140

1145

1150

Phe Ser Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg

1155

1160

1165

Asp Pro

1170

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<211> 838

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35).. (568)

<400> 101

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Met Ser Gly Gly Lys Tyr Val

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gac tcg gag gga cat ctc tac acc gtt ccc atc cgg gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

10

15

20

atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag 151  
 Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys  
 25 30 35  
 caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac 199  
 Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp  
 40 45 50 55  
 cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg 247  
 Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val  
 60 65 70  
 att gca gaa cca gaa ggg aca cac agt ttt cac ggc att tgg aag gcc 295  
 Ile Ala Glu Pro Glu Gly Thr His Ser Phe His Gly Ile Trp Lys Ala  
 75 80 85  
 agc ttc acc acc ttc act gtg acg aaa tac tgg ttt tac cgc ttg ctg 343  
 Ser Phe Thr Thr Phe Thr Val Thr Lys Tyr Trp Phe Tyr Arg Leu Leu  
 90 95 100  
 tct gcc ctc ttt ggc atc ccg atg gca ctc atc tgg ggc att tac ttc 391  
 Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe  
 105 110 115  
 gcc att ctc tct ttc ctg cac atc tgg gca gtt gta cca tgc att aag 439  
 Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys  
 120 125 130 135  
 agc ttc ctg att gag att cag tgc acc agc cgt gtc tat tcc atc tac 487  
 Ser Phe Leu Ile Glu Ile Gln Cys Thr Ser Arg Val Tyr Ser Ile Tyr  
 140 145 150  
 gtc cac acc gtc tgt gac cca ctc ttt gaa gct gtt ggg aaa ata ttc 535  
 Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe

155 160 165  
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Ser Asn Val Arg Ile Asn Leu Gln Lys Glu Ile  
170 175  
gaagtatacc tgattttttt tccitttaat tticcctggcg ccaattticaa gtccaagtt 648  
gctaatacag caacgaattt atgaattgaa ttaatcttggc tgaataataa aagaicactt 708  
tctcagtttt cataagtatt atgtctcttc tgagctatct catctatctt tggcagictg 768  
aatttttaaa acccatttat atttctttcc ttaccttttt atttgcattg ggaatcaacca 828  
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<211> 178

<212> PRT

<213> Homo sapiens

<400> 102

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Pro Ile Arg Glu Gln Gly Asn Ile Tyr Lys Pro Asn Asn Lys Ala Met

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Ala Asp Glu Leu Ser Glu Lys Gln Val Tyr Asp Ala His Thr Lys Glu

35 40 45

Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp Asp Val Val

50 55 60

Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser

65 70 75 80

Phe His Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys

85 90 95



Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala

100

105

110

Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp

115

120

125

Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Thr

130

135

140

Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe

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Glu Ala Val Gly Lys Ile Phe Ser Asn Val Arg Ile Asn Leu Gln Lys

165

170

175

Glu Ile

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<222> (1).. (444)

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ctg ttc ctc acc atc cct ttc gcc ttc ttc ctg ccc gag ctg ata ttt 96

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20

25

30

ggg ttc ttg gtc tgg acc atg gta gcc gcc acc cac ata gta tac ccc 144

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro  
           35                    40                    45  
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 Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile  
           50                    55                    60  
 tcc ttg atg ttc ctg ttg tct tac ttg ttt gga ttt tac aaa aga ttt 240  
 Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe  
           65                    70                    75                    80  
 gaa tcc tgg aga gtt ctg gac agc ctg tac cac ggg acc act ggc atc 288  
 Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile  
                     85                    90                    95  
 ctg tac atg agc gct gcc gtc cta caa gta cat gcc acg att gtt tct 336  
 Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser  
                     100                    105                    110  
 gag aaa ctg ctg gac cca aga att tac tac att aat tgc gca gcc tgc 384  
 Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser  
                     115                    120                    125  
 ttc ttc gcc ttc atc gcc acg ctg ctc tac att ctc cat gcc ttc agc 432  
 Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser  
                     130                    135                    140  
 atc tat tac cac tgatgcacag gcgccaggcc aagggggaaa tgctcttga 484  
 Ile Tyr Tyr His  
 145  
 aagctccaat tatgtgtccc caaaagcagc ttccaacgtt tgccatctgg atgacaaacg 544  
 gaagatccac taaaacgtcc acgggattaa cagaacgtcc ttgcagactg agcgatgaca 604  
 ccacactttg ttggacatt taaattcact ctgctgaata ggaggaagct ttctttttc 664  
 ctgggaaaac aactgtctct tggaattatc tgaccatgaa ctgtctcttc tagacaactc 724

acatcaaagc cctcactcca ctaatggaga atccatagccc cactaatgcc aagtcctgitt 784  
 ggggattitg cctcagclat gggcticcct agagiaggic taggggaata ctcagictga 844  
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 gctggagatgc agtgacgcga tctccactca ctgcaggctc cgccctcccg gttcccgcca 964  
 ttctcctgcc tcagccctccc gagtagccgg gactacaggc gccaccacc atgcccggct 1024  
 aatttagitg tatttttagt agagatgggg ttccaccgta ttagccagga tggctctgat 1084  
 ctccigacct cgigatccgc ccgctcggc ctcccaaagi gctgggatta caggcgtgag 1144  
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 ggtagacgtg tggggaaaat aatcattat acagtaagac ctggggcttg aggggtgggg 1444  
 aatggggagg gaagggcata gctgtcctt ccatgagtct gacatctcgg aaactgagca 1504  
 gctgccggac gctgggtca ggaatccaag accccacctc ttaaggactg gttcctcaga 1564  
 aagcacctc agggaaaaag gtgaaaacat tacatccgtg gattcctctg ccacaaccgc 1624  
 attggaagaa aaggctgccg caacatctca gcgaggagtg aaggacccat gtcccaggaa 1684  
 ccgcctcgc ccaccgcac tcacccccct cacattctct taagcaccg gttgcccctc 1744  
 gaggcctggc gaatgggtt gccacgggg ttgggcaagg gctcaccagg acctcaacgg 1804  
 gcaaagtigt gcacactaaa atatcaaatc aaggctgtt gttttaaagt aaatgttttt 1864  
 ctaaagaaag ctgigtctt ctgttgacc agacgaatag ggcacagccc tgtaactgca 1924  
 cgtgccctct gtcattggga atgaaataaa ttattacgag aaagggactt gtcctaactg 1984  
 gtttgaggcc ttacagtitt gtatctacat tttccctc ctggggtttg cggggacagg 2044  
 gacagaacta caggagtcac gggaaagaaa attctggctt cactactgct cactgctcac 2104  
 tttctgatca ctctgatact ttttttttt ttttttttt gcaacctgat accttgaaaa 2164  
 gcttctatgt gctctcctt ttgttcctg gcagctgtct aggatgatca ctgattacta 2224  
 ttactaagt agccacatgc aaataaaaagt tgtttggtaa aatgg 2269

&lt;210&gt; 104

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1 5 10 15

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20 25 30

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

35 40 45

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

50 55 60

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65 70 75 80

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

85 90 95

Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

100 105 110

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

115 120 125

Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser

130 135 140

Ile Tyr Tyr His

145

&lt;210&gt; 105

&lt;211&gt; 2899

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (91).. (2196)

&lt;400&gt; 105

gaictgaatt cggccccagc tagagctcca ggcggcgctc aggccccact cgacctctc 60  
 gggcctcggc tacttggact gcggcggaat atg gcg gct ccg atg act ccc gcg 114

Met Ala Ala Pro Met Thr Pro Ala

1

5

gct cgg ccc gag gac tac gag gcg gcg ctg aat gcc gcc ctg gct gac 162  
 Ala Arg Pro Glu Asp Tyr Glu Ala Ala Leu Asn Ala Ala Leu Ala Asp

10

15

20

gtg ccc gaa ctg gcc aga ctg ctg gag atc gac ccg tac ttg aag ccc 210  
 Val Pro Glu Leu Ala Arg Leu Leu Glu Ile Asp Pro Tyr Leu Lys Pro

25

30

35

40

tac gcc gtg gac ttc cag cgc agg tat aag cag ttt agc caa att ttg 258  
 Tyr Ala Val Asp Phe Gln Arg Arg Tyr Lys Gln Phe Ser Gln Ile Leu

45

50

55

aag aac att gga gaa aat gaa ggt ggt att gat aag ttt tcc aga ggc 306  
 Lys Asn Ile Gly Glu Asn Glu Gly Gly Ile Asp Lys Phe Ser Arg Gly

60

65

70

tat gaa tca ttt ggc gtc cac aga tgt gct gat ggt ggt tta tac tcc 354  
 Tyr Glu Ser Phe Gly Val His Arg Cys Ala Asp Gly Gly Leu Tyr Ser

75

80

85

aaa gaa tgg gcc ccg gga gca gaa gga gtt ttt ctt act gga gat ttt 402  
 Lys Glu Trp Ala Pro Gly Ala Glu Gly Val Phe Leu Thr Gly Asp Phe  
           90                          95                          100  
 aat ggt tgg aat cca ttt tcg tac cca tac aaa aaa ctg gat tat gga 450  
 Asn Gly Trp Asn Pro Phe Ser Tyr Pro Tyr Lys Lys Leu Asp Tyr Gly  
 105                          110                          115                          120  
 aaa tgg gag ctg tat atc cca cca aag cag aat aaa tct gta ctc gtg 498  
 Lys Trp Glu Leu Tyr Ile Pro Pro Lys Gln Asn Lys Ser Val Leu Val  
                           125                          130                          135  
 cct cat gga tcc aaa tta aag gta gtt att act agt aaa agc gga gag 546  
 Pro His Gly Ser Lys Leu Lys Val Val Ile Thr Ser Lys Ser Gly Glu  
                           140                          145                          150  
 atc ttg tat cgt att tca ccg tgg gca aag tat gtg gtt cgt gaa ggt 594  
 Ile Leu Tyr Arg Ile Ser Pro Trp Ala Lys Tyr Val Val Arg Glu Gly  
                           155                          160                          165  
 gat aat gtg aat tat gat tgg ata cac tgg gat cca gaa cac tca tat 642  
 Asp Asn Val Asn Tyr Asp Trp Ile His Trp Asp Pro Glu His Ser Tyr  
                           170                          175                          180  
 gag ttt aag cat tcc aga cca aag aag cca cgg agt cta aga att tat 690  
 Glu Phe Lys His Ser Arg Pro Lys Lys Pro Arg Ser Leu Arg Ile Tyr  
 185                          190                          195                          200  
 gaa tct cat gtg gga att tct tcc cat gaa gga aaa gta gct tct tat 738  
 Glu Ser His Val Gly Ile Ser Ser His Glu Gly Lys Val Ala Ser Tyr  
                           205                          210                          215  
 aaa cat ttt aca tgc aat gta cta cca aga atc aaa ggc ctt gga tac 786  
 Lys His Phe Thr Cys Asn Val Leu Pro Arg Ile Lys Gly Leu Gly Tyr  
                           220                          225                          230

aac tgc att cag ttg atg gca atc atg gag cat gct tac tat gcc agc 834  
 Asn Cys Ile Gln Leu Met Ala Ile Met Glu His Ala Tyr Tyr Ala Ser  
 235 240 245  
 ttt ggt tac caa atc aca agc ttc ttt gca gct tcc agc cgt tat gga 882  
 Phe Gly Tyr Gln Ile Thr Ser Phe Phe Ala Ala Ser Ser Arg Tyr Gly  
 250 255 260  
 aca cct gaa gag cta caa gaa ctg gta gac aca gct cat tcc atg ggt 930  
 Thr Pro Glu Glu Leu Gln Glu Leu Val Asp Thr Ala His Ser Met Gly  
 265 270 275 280  
 atc ata gtc ctc tta gat gtg gla cac agc cat gct tca aaa aat tca 978  
 Ile Ile Val Leu Leu Asp Val Val His Ser His Ala Ser Lys Asn Ser  
 285 290 295  
 gca gat gga ttg aat atg ttt gat ggg aca gat tcc tgt tat ttt cat 1026  
 Ala Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His  
 300 305 310  
 tct gga cct aga ggg act cat gat ctt tgg gat agc aga ttg ttt gcc 1074  
 Ser Gly Pro Arg Gly Thr His Asp Leu Trp Asp Ser Arg Leu Phe Ala  
 315 320 325  
 tac tcc agc tgg gaa gtt tta aga ttc ctt ctg tca aac ata aga tgg 1122  
 Tyr Ser Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ile Arg Trp  
 330 335 340  
 tgg ttg gaa gaa tat cgc ttt gat gga ttt cgt ttt gat ggt gtt acg 1170  
 Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr  
 345 350 355 360  
 tcc atg ctt tat cat cac cat gga gtg ggt caa ggt ttc tca ggt gat 1218  
 Ser Met Leu Tyr His His His Gly Val Gly Gln Gly Phe Ser Gly Asp

365	370	375	
tac agt gaa tat ttc gga cta caa gla gat gaa gat gcc ttg act tac	1266		
Tyr Ser Glu Tyr Phe Gly Leu Gln Val Asp Glu Asp Ala Leu Thr Tyr			
380	385	390	
ctc atg ttg gca aat cat ttg gtt cac acg ctg tgt ccc gat tct ata	1314		
Leu Met Leu Ala Asn His Leu Val His Thr Leu Cys Pro Asp Ser Ile			
395	400	405	
aca ata gct gag gat gta tca gga atg cca gct ctg tgc tct cca att	1362		
Thr Ile Ala Glu Asp Val Ser Gly Met Pro Ala Leu Cys Ser Pro Ile			
410	415	420	
tcc cag gga ggg ggt ggt ttt gac tat cga cta gcc atg gca att cca	1410		
Ser Gln Gly Gly Gly Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro			
425	430	435	440
gat aag tgg att cag cta ctt aaa gag ttt aaa gat gaa gac tgg aac	1458		
Asp Lys Trp Ile Gln Leu Leu Lys Glu Phe Lys Asp Glu Asp Trp Asn			
445	450	455	
atg ggc gat ata gla tac acg ctc aca aac agg cgc tac ctt gaa aag	1506		
Met Gly Asp Ile Val Tyr Thr Leu Thr Asn Arg Arg Tyr Leu Glu Lys			
460	465	470	
tgc att gct tat gca gag agc cat gat cag gca ttg gtt ggg gat aag	1554		
Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys			
475	480	485	
tcg ctg gca ttt tgg ttg atg gat gcc gaa atg tat aca aac atg agt	1602		
Ser Leu Ala Phe Trp Leu Met Asp Ala Glu Met Tyr Thr Asn Met Ser			
490	495	500	
gtc ctg act cct ttt act cca gtt att gat cgt gga ata cag ctt cat	1650		
Val Leu Thr Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His			



505	510	515	520	
aaa atg att cga ctc att acg cat ggg ctt ggt gga gaa ggc tat ctc	1698			
Lys Met Ile Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu				
525	530	535		
aat ttc atg ggt aat gaa ttt ggg cat cct gaa tgg tta gac ttc cca	1746			
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro				
540	545	550		
aga aaa gga aat aat gag agt tac cat tat gcc agg cgg cag ttt cat	1794			
Arg Lys Gly Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His				
555	560	565		
tta act gac gac gac ctt ctt cgc tac aag ttc cta aat aat ttt gac	1842			
Leu Thr Asp Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp				
570	575	580		
agg gat atg aat aga tlg gaa gaa aga tat ggt tgg ctt gca gct cca	1890			
Arg Asp Met Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro				
585	590	595	600	
cag gcc tac gtg agt gaa aaa cat gaa ggc aat aag atc att gct ttt	1938			
Gln Ala Tyr Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe				
605	610	615		
gaa aga gca ggt ctt ctt ttc att ttc aac ttc cat cca agc aag agc	1986			
Glu Arg Ala Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser				
620	625	630		
tac act gac tac cga gtt gga aca gca tlg cca ggg aaa ttc aaa att	2034			
Tyr Thr Asp Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile				
635	640	645		
glg cta gat tca gat gca gcg gaa tat gga ggg cat cag aga ctg gac	2082			

Val Leu Asp Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp  
 650 655 660  
 cac agc act gac ttt ttt tct gag gct ttt gaa cat aat ggg cgt ccc 2130  
 His Ser Thr Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro  
 665 670 675 680  
 tat tct ctt ttg gtg tac att cca agc aga gtg gcc ctc atc ctt cag 2178  
 Tyr Ser Leu Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln  
 685 690 695  
 aat gtg gat ctg ccg aat tgaagaggcc tgatttcagc tccaccagat 2226  
 Asn Val Asp Leu Pro Asn  
 700  
 gcagatttgt gttttgtttt ctgtttatca ctgtcacaca gcttataaca tgtatgcttt 2286  
 tcagaatata gtgtctagc caagccatca agtgtctgaa attcaatatt ggtttatgca 2346  
 aatcacgaa acttttattt aagtagatag gagaatatgt ttaaaatatt aggaatccta 2406  
 gaccataatt tcaagtcac ttagcagcta ggattctcaa atggaagtgt tataatataat 2466  
 atgtataaaa cattttgctt tcttggttaa ttatttgatc cttttaaatc caaatttgaa 2526  
 tcatttgtca tgtatgatta ttctgttaa atgtacacag tatttaagat ggatatttgg 2586  
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 gtctcttttt ttcaaattgt gtttagaaat actgtaataa atatgcagta gtgatataaa 2706  
 gaattatac caaggtaata taaaagccat tacgtatgaa ctcatccgtg tctcatittg 2766  
 tgttttattt tglgactct tgtccactaa gtatcttgtt aaatgccagt atctcagict 2826  
 ttctgaagcc ctgaaatggt aattgtagca ttccagaaaa tgtctttcat ttcaatcaat 2886  
 aaaaagcttt tgt 2899

&lt;210&gt; 106

&lt;211&gt; 702

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

Met Ala Ala Pro Met Thr Pro Ala Ala Arg Pro Glu Asp Tyr Glu Ala

1 5 10 15

Ala Leu Asn Ala Ala Leu Ala Asp Val Pro Glu Leu Ala Arg Leu Leu

20 25 30

Glu Ile Asp Pro Tyr Leu Lys Pro Tyr Ala Val Asp Phe Gln Arg Arg

35 40 45

Tyr Lys Gln Phe Ser Gln Ile Leu Lys Asn Ile Gly Glu Asn Glu Gly

50 55 60

Gly Ile Asp Lys Phe Ser Arg Gly Tyr Glu Ser Phe Gly Val His Arg

65 70 75 80

Cys Ala Asp Gly Gly Leu Tyr Ser Lys Glu Trp Ala Pro Gly Ala Glu

85 90 95

Gly Val Phe Leu Thr Gly Asp Phe Asn Gly Trp Asn Pro Phe Ser Tyr

100 105 110

Pro Tyr Lys Lys Leu Asp Tyr Gly Lys Trp Glu Leu Tyr Ile Pro Pro

115 120 125

Lys Gln Asn Lys Ser Val Leu Val Pro His Gly Ser Lys Leu Lys Val

130 135 140

Val Ile Thr Ser Lys Ser Gly Glu Ile Leu Tyr Arg Ile Ser Pro Trp

145 150 155 160

Ala Lys Tyr Val Val Arg Glu Gly Asp Asn Val Asn Tyr Asp Trp Ile

165 170 175

His Trp Asp Pro Glu His Ser Tyr Glu Phe Lys His Ser Arg Pro Lys

180 185 190

Lys Pro Arg Ser Leu Arg Ile Tyr Glu Ser His Val Gly Ile Ser Ser

195	200	205	
His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu			
210	215	220	
Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile			
225	230	235	240
Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe			
245	250	255	
Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu			
260	265	270	
Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val			
275	280	285	
His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp			
290	295	300	
Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp			
305	310	315	320
Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg			
325	330	335	
Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp			
340	345	350	
Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly			
355	360	365	
Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln			
370	375	380	
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val			
385	390	395	400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly			

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405 410 415  
 Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Gly Phe Asp  
 420 425 430  
 Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys  
 435 440 445  
 Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu  
 450 455 460  
 Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His  
 465 470 475 480  
 Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp  
 485 490 495  
 Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val  
 500 505 510  
 Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His  
 515 520 525  
 Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly  
 530 535 540  
 His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr  
 545 550 555 560  
 His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg  
 565 570 575  
 Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu  
 580 585 590  
 Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His  
 595 600 605  
 Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile  
 610 615 620

Phe Asn Phe His Pro Ser Lys Ser Tyr Thr Asp Tyr Arg Val Gly Thr  
 625                      630                      635                      640  
 Ala Leu Pro Gly Lys Phe Lys Ile Val Leu Asp Ser Asp Ala Ala Glu  
                          645                      650                      655  
 Tyr Gly Gly His Gln Arg Leu Asp His Ser Thr Asp Phe Phe Ser Glu  
                          660                      665                      670  
 Ala Phe Glu His Asn Gly Arg Pro Tyr Ser Leu Leu Val Tyr Ile Pro  
                          675                      680                      685  
 Ser Arg Val Ala Leu Ile Leu Gln Asn Val Asp Leu Pro Asn  
                          690                      695                      700

<210> 107

<211> 790

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78).. (626)

<400> 107

acigccccc aa ggcccccgcc gccgcicccag cgccgcgcag ccaccgccgc cgccgcgcgc 60  
 tciccttagt cgccgcc atg acg acc gcg tcc acc tcg cag gtg cgc cag 110  
                          Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln  
                          1                      5                      10  
 aac tac cac cag gac tca gag gcc gcc atc aac cgc cag atc aac ctg 158  
 Asn Tyr His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu  
                          15                      20                      25  
 gag ctc tac gcc tcc tac gtt tac ctg tcc atg tct tac tac ttt gac 206

Glu Leu Tyr Ala Ser Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp  
 30 35 40  
 cgc gat gat gtg gct ttg aag aac ttt gcc aaa tac ttt ctt cac caa 254  
 Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln  
 45 50 55  
 tct cat gag gag agg gaa cat gct gag aaa ctg atg aag ctg cag aac 302  
 Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn  
 60 65 70 75  
 caa cga ggt ggc cga atc ttc ctt cag gat atc aag aaa cca gac tgt 350  
 Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys  
 80 85 90  
 gat gac tgg gag agc ggg ctg aat gca atg gag tgt gca tta cat ttg 398  
 Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu  
 95 100 105  
 gaa aaa aat gtg aat cag tca cta ctg gaa ctg cac aaa ctg gcc act 446  
 Glu Lys Asn Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr  
 110 115 120  
 gac aaa aat gac ccc cat ttg tgt gac ttc att gag aca cat tac ctg 494  
 Asp Lys Asn Asp Pro His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu  
 125 130 135  
 aat gag cag gtg aaa gcc atc aaa gaa ttg ggt gac cac gtg acc aac 542  
 Asn Glu Gln Val Lys Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn  
 140 145 150 155  
 ttg cgc aag atg gga gcg ccc gaa tct ggc ttg gcg gaa tat ctc ttt 590  
 Leu Arg Lys Met Gly Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe  
 160 165 170

gac aag cac acc cag gga gac agt gat aat gaa agc taagccctcgg 636

Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser

175

180

gctaatttcc ccatagccgi ggggtgactt ccciggtcac caaggcagtg catgcatggt 696

ggggtttcct ttaccttttc tataagtgtg accaaaacat ccacttaagt tctttgattt 756

gtaccattcc ttcaaataaa gaaatttggg accc 790

<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

<400> 108

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln Asn Tyr His Gln Asp

1

5

10

15

Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser

20

25

30

Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp Arg Asp Asp Val Ala

35

40

45

Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg

50

55

60

Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn Gln Arg Gly Gly Arg

65

70

75

80

Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys Asp Asp Trp Glu Ser

85

90

95

Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu Glu Lys Asn Val Asn

100

105

110

Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn Asp Pro



115                      120                      125  
 His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys  
 130                      135                      140  
 Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly  
 145                      150                      155                      160  
 Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe Asp Lys His Thr Leu  
 165                      170                      175  
 Gly Asp Ser Asp Asn Glu Ser

180

&lt;210&gt; 109

&lt;211&gt; 3460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (256).. (1857)

&lt;400&gt; 109

ccctaccgcc cccaattccg cccgtccccc gccgcggcgg cgctagccgc cactgaggga 60  
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 gggctgggct gtgcgccigc gcagtgtggg tcgctccga ttcctgccc cggccggccc 180  
 cgctcggct ccgcacccic gcccgcctc cagccgccgc tctgccccgc agcagccagc 240  
 cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys

1

5

10

aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339  
 Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu

15	20	25	
tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag	387		
Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu			
30	35	40	
ttc cac tcg ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg	435		
Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met			
45	50	55	60
gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga	483		
Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg			
65	70	75	
cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc	531		
His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro			
80	85	90	
acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg	579		
Thr Thr Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val			
95	100	105	
gtg ccg ggc aac gcg ctc gtg glg gac ccg cgg cgc ccc ttc cgc aag	627		
Val Pro Gly Asn Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys			
110	115	120	
ctc aac gcg ttt ggc aac gct ttc ctc aac agg ttc atg tgt gcc cag	675		
Leu Asn Ala Phe Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln			
125	130	135	140
ctg ccc aac ccc gtc ctg gac agc atc agc atc atc gac acc ccc ggg	723		
Leu Pro Asn Pro Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly			
145	150	155	
atc ctg tct gga gag aag cag cgg atc agc aga ggc tat gac ttt gca	771		
Ile Leu Ser Gly Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala			

160	165	170	
gcc gtc ctg gag tgg ttc gcg gag cgt gtg gac cgc atc atc ctg ctc	819		
Ala Val Leu Glu Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu			
175	180	185	
ttc gac gcc cac aag ctg gac atc tcc gat gag ttc tcg gaa gtg atc	867		
Phe Asp Ala His Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile			
190	195	200	
aag gct ctg aag aac cat gag gac aag atc cgc gtg gtg ctg aac aag	915		
Lys Ala Leu Lys Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys			
205	210	215	220
gca gac cag atc gag acg cag cag ctg atg cgg gtg tac ggg gcc ctc	963		
Ala Asp Gln Ile Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu			
225	230	235	
atg tgg tcc ctg ggc aag atc atc aac acc ccc gag gtg gtc agg gtc	1011		
Met Trp Ser Leu Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val			
240	245	250	
tac atc ggc tcc ttc tgg tcc cac ccg ctc ctc atc ccc gac aac cgc	1059		
Tyr Ile Gly Ser Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg			
255	260	265	
aag ctc ttt gag gcc gag gag cag gac ctc ttc aag gac atc cag tca	1107		
Lys Leu Phe Glu Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser			
270	275	280	
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg	1155		
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg			
285	290	295	300
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa	1203		

Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys  
 305 310 315  
 gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg 1251  
 Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val  
 320 325 330  
 aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc 1299  
 Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile  
 335 340 345  
 tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag 1347  
 Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln  
 350 355 360  
 acc cag gac ttc agc aag ttc cag gcg ctg aag ccc aag ctg ctg gac 1395  
 Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp  
 365 370 375 380  
 acg gtg gat gac atg ctg gcc aac gac atc gcg cgg ctg atg gtg atg 1443  
 Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met  
 385 390 395  
 gtg cgg cag gag gag tcc ctg atg cct tcc cag gtg gtc aag ggc ggc 1491  
 Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly  
 400 405 410  
 gcc ttt gac ggc acc atg aac ggg ccg ttc ggg cac ggc tac ggc gag 1539  
 Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu  
 415 420 425  
 ggg gcc ggc gag ggc atc cac gac gtg gag tgg gtg gtg ggc aag gac 1587  
 Gly Ala Gly Glu Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp  
 430 435 440  
 aag ccc acc tac gac gag atc ttc tac acg ctg tcc cct gtc aac ggc 1635

Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly  
 445                      450                      455                      460  
 aag atc acg ggc gcc aac gcc aag aag gag atg gig aag tcc aag ctc 1683  
 Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu  
                          465                      470                      475  
 ccc aac acc gtg cta ggg aag atc tgg aag ctg gcc gac gtg gac aag 1731  
 Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys  
                          480                      485                      490  
 gac ggg ctg ctg gac gac gag gag ttc gcg ctg gcc aac cac ctc atc 1779  
 Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile  
                          495                      500                      505  
 aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac 1827  
 Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His  
                          510                      515                      520  
 ctg gtg ccg ccc tcc aag cgc aga cat gag tgatggcgcc cggccccgca 1877  
 Leu Val Pro Pro Ser Lys Arg Arg His Glu  
 525                      530  
 cctgccattt gcacgcccgg ccgggaggca gagacggggg gaggggaagc ctcaccattt 1937  
 ctcaaggtcc ataaagactg agcggatgtt tctcgcctc tcgaaaagga aaaccacat 1997  
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 ctctatttcc taccttctt cctcctctgt ttagcaaagg agggcagctc acttggatgt 3017  
 ccttacaacg cccctggccc caggttgagc aataagaaac cagaacctg cgcccagtg 3077  
 gcccgggcca gttcaggccg cctccccctc ctctgccttg ggccatigag cccagcctc 3137  
 caggggcccc ggtgcgttgc caagccagtg gccactgtcc gggctlgat ggcaccaagg 3197  
 caggttgagc accaggtacc acacagctgg gcttcccacc aggccttccc gcgggggtct 3257  
 cagggagctt cccccagcg ctgctggag tctgcaggaa ctggccttgt tctcttagc 3317  
 ccgtactcc alacagtatt aggtgaggat ggatgcgggc gctgtccttg ccgggaagtc 3377  
 actgtgaag ttgcagtggc ttgttcacac ctgtgggaag agaagtgaag actttctctt 3437  
 tgcatlaaaa agtctgaact gtg 3460

<210> 110

<211> 534

<212> PRT

<213> Homo sapiens

<400> 110

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys Lys Glu Pro Glu

1

5

10

15

Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu Tyr Ala Gln Lys

	20	25	30
Leu	Leu	Pro	Leu
Glu	Glu	His	Tyr
Arg	Phe	His	Glu
Phe	His	Ser	Pro
	35	40	45
Xaa	Leu	Glu	Asp
Ala	Asp	Phe	Asp
Asn	Lys	Pro	Met
Val	Leu	Leu	Val
	50	55	60
Xaa	Gln	Tyr	Ser
Thr	Gly	Lys	Thr
Thr	Phe	Ile	Arg
His	Leu	Ile	Glu
	65	70	75
Gln	Asp	Phe	Pro
Gly	Met	Arg	Ile
Gly	Pro	Glu	Pro
Thr	Thr	Asp	Ser
	85	90	95
Phe	Ile	Ala	Val
Met	His	Gly	Pro
Thr	Glu	Gly	Val
Val	Pro	Gly	Asn
	100	105	110
Ala	Leu	Val	Val
Asp	Pro	Arg	Arg
Pro	Phe	Arg	Lys
Leu	Asn	Ala	Phe
	115	120	125
Gly	Asn	Ala	Phe
Leu	Asn	Arg	Phe
Met	Cys	Ala	Gln
Leu	Pro	Asn	Pro
	130	135	140
Val	Leu	Asp	Ser
Ile	Ser	Ile	Ile
Asp	Thr	Pro	Gly
Ile	Leu	Ser	Gly
	145	150	155
Glu	Lys	Gln	Arg
Ile	Ser	Arg	Gly
Tyr	Asp	Phe	Ala
Ala	Val	Leu	Glu
	165	170	175
Trp	Phe	Ala	Glu
Arg	Val	Asp	Arg
Ile	Ile	Leu	Leu
Phe	Asp	Ala	His
	180	185	190
Lys	Leu	Asp	Ile
Ser	Asp	Glu	Phe
Ser	Glu	Val	Ile
Lys	Ala	Leu	Lys
	195	200	205
Asn	His	Glu	Asp
Lys	Ile	Arg	Val
Val	Leu	Asn	Lys
Ala	Asp	Gln	Ile
	210	215	220
Glu	Thr	Gln	Gln
Leu	Met	Arg	Val
Tyr	Gly	Ala	Leu
Met	Trp	Ser	Leu
	225	230	235
			240

Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser  
                     245                    250                    255  
 Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu  
                     260                    265                    270  
 Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn  
                     275                    280                    285  
 Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala  
                     290                    295                    300  
 Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn  
 305                    310                    315                    320  
 Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly  
                     325                    330                    335  
 Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp  
                     340                    345                    350  
 Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe  
                     355                    360                    365  
 Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp  
                     370                    375                    380  
 Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu  
 385                    390                    395                    400  
 Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly  
                     405                    410                    415  
 Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu  
                     420                    425                    430  
 Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr  
                     435                    440                    445



Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly

450

455

460

Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val

465

470

475

480

Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu

485

490

495

Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu

500

505

510

Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro

515

520

525

Ser Lys Arg Arg His Glu

530

&lt;210&gt; 111

&lt;211&gt; 1622

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (89).. (724)

&lt;400&gt; 111

ggtcggtgtg ctlttgaccc tgcctttgtg tggctgtcac cggtagggact ggcggggact 60

gtgtgattaa cctccatttc agctaatac atg gga gag att aaa gtc tct cct 112

Met Gly Glu Ile Lys Val Ser Pro

1

5

gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg 160

Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val

10	15	20	
gat gat gat gac agt aag ata tgg tgc ctc tat gac gcg ggc ccc cga			208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg			
25	30	35	40
agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca			256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala			
45	50	55	
gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg			304
Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg			
60	65	70	
gtt atc gct ttg cag tat cca gtt tat tgg gac cat ctc gag ttc tgt			352
Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys			
75	80	85	
gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat			400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His			
90	95	100	
ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa			448
Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu			
105	110	115	120
tac act cac aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc			496
Tyr Thr His Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser			
125	130	135	
ttc agt gac acc tct atc ttc aac caa act tgg act gca aac agc ttt			544
Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe			
140	145	150	
tgg ctg atg cct gca ttt atg ctc aaa aaa ata gtt ctt gga aat ttt			592
Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe			

155	160	165	
tca tct ggc ccg gtg gac cct atg atg gct gat gcc att gat ttc atg	640		
Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met			
170	175	180	
gta gac agg cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt	688		
Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu			
185	190	195	200
acc ttg aaa ttg tca aaa ttc tta tgt gga acc tca taaaattcgg	734		
Thr Leu Lys Leu Ser Lys Phe Leu Cys Gly Thr Ser			
205	210		
ggacatacct gtaactatta tggatgtgtt tgatcagagt gcgcittcaa ctgaagctaa	794		
agaagaaaatg tacaagctgt atccctaattg ccccgaagag gctcatctga aaacaggagg	854		
caatttccca taccigigca gaagtgcaga ggicaatctt tatgtacaga tacatttgtc	914		
kgcaattccw kggrggaccm aatacgcggc ctttgaccca tcaatggtea glgcccagga	974		
gcctgagggtg cagaaaggca gccttggcat cagccaggag gagcagtagt gtgtctctcg	1034		
ctgtcaatga tgagttgacc cgggtgtgtc ttgtatagtc agtgggcatc agcaccggtt	1094		
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ctttggtttt cttagctttt gaatttgaag aagtactttt gaagactccc attttaagaa	1274		
ccgtgcaaat ttgctacca aaagcttca ccaactgtgt cttaagttaa tgttaatttc	1334		
tgaggtttgg gactttgtgg tggttttttt cttcttttct tttccattct tctttctttc	1394		
tttttatgtt gtttgcigta aatgcctcac atccagattg catatcagga cattggttat	1454		
tttatgcttt ctggatata accatgatca gagtgccatg gccactaccc cactgtttgc	1514		
tctcctgcaa atcaactgct tttaatctac acttaaacaa attgttttga gtgttagcta	1574		
ctgcccttct agataattagt catttggaaat aaaaattcaa tttcactg	1622		

&lt;210&gt; 112

WO 01/25427

&lt;211&gt; 212

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr  
 1 5 10 15  
 Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp  
 20 25 30  
 Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe  
 35 40 45  
 Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu  
 50 55 60  
 Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val  
 65 70 75 80  
 Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp  
 85 90 95  
 His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly  
 100 105 110  
 Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val  
 115 120 125  
 His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn  
 130 135 140  
 Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu  
 145 150 155 160  
 Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met  
 165 170 175

WO 01/25427

Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly

180

185

190

Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Lys Leu Ser Lys Phe Leu

195

200

205

Cys Gly Thr Ser

210

&lt;210&gt; 113

&lt;211&gt; 2391

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (360)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (49)

&lt;223&gt; g or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (51)

&lt;223&gt; a or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (54)

&lt;223&gt; t or c

&lt;220&gt;

WO 01/25427

&lt;221&gt; unsure

&lt;222&gt; (55)

&lt;223&gt; g or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (56)

&lt;223&gt; g or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (91)

&lt;223&gt; g or c

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (101)

&lt;223&gt; t or c

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (103)

&lt;223&gt; g or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (325)

&lt;223&gt; t or c

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (425)

&lt;223&gt; g or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (688)

&lt;223&gt; g or c

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1459)

&lt;223&gt; g or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1705)

&lt;223&gt; g or t

&lt;400&gt; 113

gac ccg ttc cat gca gtt gta tac ata gig ttc atg ctc ggc tcc tgt 48

Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

1 5 10 15

kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa 96

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20 25 30

gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac 144

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35 40 45

cga gag acc tcc atg gtc cat gaa ctc aac cgg tac atc ccc aca gcc 192

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50 55 60

gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctc tgc gtc ctg gct gac 240

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp  
65 70 75 80  
ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca 288  
Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr  
85 90 95  
atc atc tac cag tac tti gag atc ttc gtt aag gag yaa agc gag gtt 336  
Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val  
100 105 110  
ggc agc atg ggg gcc ctg ctc ttc tgagcccgct tcccgacag gttaggaag 390  
Gly Ser Met Gly Ala Leu Leu Phe  
115 120  
ctgctccaga agcgctcgg aaggggagct ctacatgg cgctgctgc tgcggcalat 450  
ggacttttaa taatgtgttt tgaatttcgt attctttcat tccactgtgt aaagtgttag 510  
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<211> 120

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<213> Homo sapiens

<220>

<221> unsure

<222> (17)

<223> unknown

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<221> unsure

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<223> unknown

<400> 114

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1 5 10 15

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20 25 30

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35 40 45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50 55 60

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp

65                      70                      75                      80  
 Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr  
                          85                      90                      95  
 Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val  
                          100                      105                      110  
 Gly Ser Met Gly Ala Leu Leu Phe  
                          115                      120

<210> 115

<211> 599

<212> DNA

<213> Homo sapiens

<400> 115

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 aatgaaagag tgacctaga gggctccttg ggctcagga atgctccgc tgcgtgaag 240  
 atgagaaggt gctcttactc agttaatgat gattgactat atttaccaaa gcccctacct 300  
 gctgctgggt ccttgttagc acaggagact tgggctaagg gcccctccca gggaaggac 360  
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 gaggactagc aggaggcagc cttgagaaac cggcagttcc caaagccagc gcctggctgt 480  
 tctctcattg tcactgccct ctccccaacc tctctctaa cccactagag attgcctgtg 540  
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<210> 116

<211> 364

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (134)

<223> a, c, g or t

<220>

<221> unsure

<222> (135)

<223> a, c, g or t

<220>

<221> unsure

<222> (179)

<223> g or a

<400> 116

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acagtgcctc caggggtgca ttgggtggaa tgagaatagt gatgaagtag aaatgtctgc 120

cacagttcca ggannggta ggtagcagtg tgtgtgttat gtgccactga ccctgaaara 180

tgtgccatag cccaagccaa ttgaaatga tcagggggcc aggcatggtg gctcatgcct 240

gtaatcccag cacttggga agctgaggtg ggaggatlgc ttgaaaccag gagttcaaga 300

ccagcctgig caacatagca aaaccccatc tctacaaaga ttaaaaataa aaaattagct 360

gggc

364

&lt;210&gt; 117

&lt;211&gt; 852

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (26).. (217)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (37)

&lt;223&gt; a, c, g or t

&lt;400&gt; 117

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Met Asp Gly Xaa Val Thr Phe Leu Thr

1

5

agc tgg gct aac ctt tcc cga act tgt ttc ccg gag gca agg tgc tcg 100

Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser

10

15

20

25

gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tcg agg cta ggg 148

Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly

30

35

40

cat tac gtt tcg tgg aac caa agc agc caa ttg cat agc aag tat ttt 196

His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe

45

50

55

cct gca ttc caa tta aat gct taagaaaaag cagcatccta taaaattgtg 247

Pro Ala Phe Gln Leu Asn Ala

60

atcataaaca tccatttccc tcagcttttg tgagtgcctt gacttacagc caacatcact 307  
 gtttaactca gtcgttttaa aaacaaactt ttctgggtgg tgataacaga gatttgctcc 367  
 ctgagccatc agggctctgg gagctggaag tgaaagggtt attaacattc taccittatg 427  
 cagctgttgg ctgaccagaa taaactccct gctgagtcca agctttaga ggaatggatg 487  
 caaatgatgt tgtttccatt agagcaggtg ctacacagcat tctgattggc ctgagcagac 547  
 cgaggctatg gctgttggga caagcttagc atcctggaca tcttgtcaaa gaacctcact 607  
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 tctccaacat ggtgtgtctg gcaggcttag gtttagaaaa tctgactgt taaaggcgtt 727  
 tgaatacatc acattcctat gcaaatgttt ttaatctcca gtttaatgta gtttattttt 787  
 cctatatgta aagtattttt atacggcttg tatcatgata gtttagcaat aaaacagttg 847  
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&lt;210&gt; 118

&lt;211&gt; 64

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (4)

&lt;223&gt; unknown

&lt;400&gt; 118

Met Asp Gly Xaa Val Thr Phe Leu Thr Ser Trp Ala Asn Leu Ser Arg

1

5

10

15

Thr Cys Phe Pro Glu Ala Arg Cys Ser Val Thr Gln Arg Ile Leu Thr

20

25

30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

35

40

45

Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

50

55

60

<210> 119

<211> 1156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (524).. (1105)

<220>

<221> unsure

<222> (10)

<223> a or t

<400> 119

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 gctagagaca gggagagcag agtaaaaccc tcaggctgct gaaatttcta ggctgttagg 180  
 aagcccctcg aattctgtga aaatgagggt ttcttaactc aactgagag cggaaagggg 240  
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 agtaaaactca agcctggcac tggctttctg ccgcttcatg tgctttggaa aaagcaggag 420  
 aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagaggga 480  
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Met Leu Lys Cys

1

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gtg gtg gtg ggg gac ggt gcc glg ggg aaa acc tgc ctg ctg atg agc 583
Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Met Ser
      5              10              15              20
tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc act gtg ttt gac 631
Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro Thr Val Phe Asp
              25              30              35
cac tat gca gtt act gtg act gtg gga ggc aag caa cac ttg ctc gga 679
His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln His Leu Leu Gly
              40              45              50
ctg tat gac acc gcg gga cag gag gac tac aac cag ctg agg cca ctc 727
Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln Leu Arg Pro Leu
              55              60              65
tec tac ccc aac acg gat gtg ttt ttg atc tgc ttc tct gtc gta aac 775
Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn
              70              75              80
cct gcc tct tac cac aat gtc cag gag gaa tgg gtc ccc gag ctc aag 823
Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val Pro Glu Leu Lys
      85              90              95              100
gac tgc atg cct cac gtg cct tat gtc ctc ata ggg acc cag att gat 871
Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly Thr Gln Ile Asp
              105              110              115
ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg tat atg aaa gag 919
Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu Tyr Met Lys Glu
              120              125              130
aaa cct ctc act tac gag cat ggt gtg aag ctc gca aaa gcg atc gga 967
Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala Lys Ala Ile Gly

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135                      140                      145  
 gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa 1015  
 Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys  
 150                      155                      160  
 gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag 1063  
 Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys Lys  
 165                      170                      175                      180  
 aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc 1105  
 Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile  
 185                      190  
 tgaggttgct tgggacctgc ctccacccca tccagggatg agaatggcag c 1156

&lt;210&gt; 120

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 120

Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys  
 1                      5                      10                      15  
 Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro  
 20                      25                      30  
 Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln  
 35                      40                      45  
 His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln  
 50                      55                      60  
 Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe  
 65                      70                      75                      80

Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val  
                     85                    90                    95  
 Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly  
                     100                    105                    110  
 Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu  
                     115                    120                    125  
 Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala  
                     130                    135                    140  
 Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln  
                     145                    150                    155                    160  
 Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His  
                     165                    170                    175  
 Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser  
                     180                    185                    190  
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<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (259)

<220>

<221> unsure

<222> (28)

<223> a, c, g or t

<220>

<221> unsure

<222> (388)

<223> g or a

<220>

<221> unsure

<222> (631)

<223> a or t

<220>

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<222> (637)

<223> g or a

<220>

<221> unsure

<222> (638)

<223> g or a

<220>

<221> unsure

<222> (639)

<223> g or a

<400> 121

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Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

acc gig tai gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc 97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20 25 30  
 ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac 145  
 Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn  
 35 40 45  
 atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg 193  
 Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala  
 50 55 60  
 ctg gct gtg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act 241  
 Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr  
 65 70 75 80  
 gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc 289  
 Val Lys Val Trp Thr Cys  
 85  
 cctgaaccag cccaggacct ttcagagcca ggcaggccac atggggtggt ctgggggttt 349  
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<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<223> unknown

<400> 122

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20

25

30

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

35

40

45

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

50

55

60

Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

65

70

75

80

Val Lys Val Trp Thr Cys

85

&lt;210&gt; 123

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (168).. (350)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (343)

&lt;223&gt; g or a

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (422)

&lt;223&gt; t or c

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (457)

&lt;223&gt; g or c

&lt;400&gt; 123

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 gccaaacttg gtigaagact aggtcttccc tggcaagttc cggaaga atg gac tta 176

Met Asp Leu

1

ctg act ttt atc aac tct tct cac tgc caa ggc caa cag cat ctg agg 224  
 Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln His Leu Arg

5

10

15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt 272  
 Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20

25

30

35

ctg tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt 320  
 Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

40

45

50

gct tca gag cct ttg cag ctg cra cct agt tgaatccaca taggsttcc 370  
 Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

55

60

tccacacggt gggaaggatc ttgctgcitt cactcacagg accaggaggat tyttcaatca 430  
 ggagggtgggt ttttgttccc ttcaggscit tggcaacatc tagagacagt ttigattgcc 490  
 acgcctggag tgggatgtgt gtgctactgg catctagtgg ctgctaaaca tctacactg 550  
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<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (59)

<223> unknown

<400> 124

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1 5 10 15

His Leu Arg Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly

20 25 30

Gly Tyr Phe Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr

35 40 45

His Cys Cys Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

50 55 60

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775).. (1017)

<220>

<221> unsure

<222> (200)

<223> g or a

<400> 125

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 catctggggg ctgagaccac ccttgccctgc ccccttcttt ctgccctaag aatgtccttt 360  
 taggctgggc atgggtgtca cgcctgtaac cccagcactt tgggaggcgg agacgggcag 420  
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Met

1

tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac 825  
 Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His

5

10

15

ggt cat acg gca ggt tgc cac aaa acc aag atg gca gcc ctt cct cag 873  
 Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln

20

25

30

cgt gcc tca ctg cca ctc cca gag cca ggg agc ccc ata aaa ccc aca 921  
 Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr

35

40

45

tca tgl ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg 969  
 Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp

50

55

60

65

gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga 1017

Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly

70

75

80

tgacagacag ctggcccgca cactcgggcc ccactcaagg atgtagggcc tttctggcc 1077

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ggggcattcac ctcttctgc tgcctcctcc tgcctctacc ctcaagggcc tgggggctgc 1197

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<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

<400> 126

Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala

1

5

10

15

His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro

20

25

30

Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro

35

40

45

Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro

50

55

60

Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu

65

70

75

80

Gly

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734).. (886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

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tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720
gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga 769

```

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

1

5

10

```

ccc tgt ctc aaa aaa aaa aaa aat ata tat ata tat ata tat tat ttt 817

```

Pro Cys Leu Lys Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe  
 15 20 25  
 tat gag gtc aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga 865  
 Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly  
 30 35 40  
 acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt 916  
 Thr Ser Trp Lys Thr Thr Pro  
 45 50  
 gattccctgct ttcagaagga ggtggattca aatacatcaa aagtccttcc ctctgctaag 976  
 tgtttatagt tcaatgaata atttcaatat ttgtatgigt tcttgctatt ttattttttt 1036  
 ctgaaaaact tccaaaaatt tgaaaataaa attacagcct tttcttctt 1085

&lt;210&gt; 128

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 128

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys  
 1 5 10 15  
 Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys  
 20 25 30  
 Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys  
 35 40 45  
 Thr Thr Pro  
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&lt;210&gt; 129

&lt;211&gt; 1544

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<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

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acaaaaaccc aattttgttc atattgaagc atgaaataaa tgagagcaag glagggccaa 180

attaactctt gtggacagtc cctaaaagtc cagtcttaca ttgtgaaaa ttgtggtgcc 240

atgaattaag atggatgact ggaaaaaggt gtggagaaa gatttaaaga tgaggaagag 300

atatttttag tataatgaagt taaccaggga ctgtatattc ataattcagt gctgtggaaa 360

tgaaaaaaat gattgaagag gtggaacgga aatgacctta gggggaaaaa aaaggaccaa 420

agaagcttga ttaaaagttg aaatcagtat ttctgaattc aaattgcttg aatttccaaa 480

atagtcagta aaggatctaa tagaaccaga attatttggg tgaattctgc aggttttatg 540

ggcttgtcac aacgtgaagg gctggaatgt atattaccaa atgggaattt ccattgtagg 600

tttttgctag tcccacccc attttagcct aatttggcct aaacgcagta tggggagaat 660

tgttccatt ccatgtgtc tgaattcagc tcatctccca gcatatagat atatctcct 720

ttaactccga ccagaacct tcttctgtg gcactccca ccatagacc ttcagatcat 780

ctcccacacc ctggatctca ctctctctt agtaacagag acactcctga ggttggactt 840

ccctgctttt ctctacttc aaatcacaat ttcttacaac caagctttgt gctcccagat 900

aagcagggat gtactagggg aatgtaaaac tgcaaaactta aaaacctgca tcttcttgaa 960

gcalcagttt tacttacaa atggtttaga gtcataagat gacctattt tatataaaag 1020

ttatattata gaataaaaig ttcatagca tagactgtta agataaaaaa ataggraatc 1080

ttgcaaggta attcttattt gcaagtgggt tatgtgttca ctctctcta cctttatggt 1140

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ctgttaacc aggccctaga ctctagtc ctctgaggca gaaccaaagg agccgcact 1260

gggggaaatc ccttttctg cctgccgtc tgccgtgac ctgtgtacgt attacaggct 1320

ttaggaccag ctgattgta tgcttgcagg atggtttga aacagaaaca atacttgttt 1380

actgtaggaa tcctatitai attatttttc agtcctgiga atgctgigaa aagatttatt 1440

cctttgaggc caggaagctc ccaggcatai atgcttctag gtiaggattg tcctgactca 1500

ctaaagaigc caggataattg gggctgaggg gagtttgagg tggt 1544

<210> 130

<211> 508

<212> DNA

<213> Homo sapiens

<400> 130

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atgggaaaca gggtatcggg ggattcatga agtcagttag agtaattgct tcttttttgc 120

gggtgaactg aatgtatttc ttcaccaaatt cttagatgta acaattaaaa agaagaaatg 180

acatgcaagt aggtcttagc agaaaaatgc aggcctgggca tgagtcatgt tgttaccctc 240

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttctigaagt tattgttagt 300

atttggtatc tcaaattttt cgtcacgtgt cacatgccac ttctctctgt cacagtggta 360

tcctcatitg ctttttaacc tacactgagg agtctttgtc aggttgcact gattttccaa 420

ttctgcagta atgagtaagc tcacggcatg gggaagaaga cagtcagtcc aatgaagttc 480

tctaaattat tttaacattg cctttgaa

508

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)

<223> g or t

<220>

<221> unsure

<222> (54)

<223> g or c

<220>

<221> unsure

<222> (300)

<223> g or c

<220>

<221> unsure

<222> (407)

<223> g or a

<220>

<221> unsure

<222> (415)



<223> a, c, g or t

<220>

<221> unsure

<222> (417)

<223> g or c

<220>

<221> unsure

<222> (419)

<223> t or c

<220>

<221> unsure

<222> (430)

<223> a or t

<220>

<221> unsure

<222> (448)

<223> t or c

<220>

<221> unsure

<222> (449)

<223> g or t

<220>

<221> unsure

<222> (472)

<223> a, c, g or t

<400> 131

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gtggccacc cttgggtcag acagctctgg gccctttgac cacaagccag cccctcgccc 180

tcctcgtggc atagcttct ctgccccagg actgcagggc ggcttctcc aaggcttcca 240

aggtcaaaa gaaatttggc tccatccaag aaggctccag ctccctact ggcccctggs 300

ttcaggccca caccctggg ccagggccag agagtgtgtc tcaggagaat tcaatgggct 360

ctagagagac acacagaaag ttggggcatt tgggaaattt tcaaggrtgt atgntsgyt 420

cacgtatggw gcaggttgc ctggctcykg ggtgcaggga agtgggctgc anggaagtgg 480

attggagggg agcttgagga atataaggag cgggggtgga gactcaggct atggacaagg 540

acagcccaa ggttgggaag acctggcctt agtcgtctc agcctagggg cagggcagt 600

aagaaagctc tccccgtcc tgcigtatg acccagagta gcctccccag gccggcatct 660

tatgtgtgtc ttccaccatc ctcatggtg cacttttcta ggctgtctc ccagcattgt 720

gcaaggctcg gaagagaacc aggaagtga aactgggtga aaacagaaag ctcaatggat 780

gggctagggtt cccagatca ttagggcaga gtttgacgt cctctggta ctggaatcca 840

cccagccac gaatcactc cctctgaag gatttatatt ctactgggtt ttggaacaaa 900

ctcctgctga gacccacag ccagaaactg aaagcagcag ctcccaaag cctggaaaat 960

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cctg 1204

<210> 132

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (223)

<223> a, c, g or t

<220>

<221> unsure

<222> (237)

<223> a, c, g or t

<220>

<221> unsure

<222> (380)

<223> a, c, g or t

<220>

<221> unsure

<222> (468)

<223> a, c, g or t

<400> 132

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acactccagc ctgggtgaca gactgagatc ctgtctcaaa aaaagagaaa gaaaaccttt 120

gagattcttc caTTTTtaga gctgagagag cacttgtgaa acacacacac atgcacaaac 180

atataaacat gcatacaggc atgcacatgc acacacaaat acncatacac acacacnagc 240

acacacacac caccaccacc atcatcagag gaacttacag aaaaggggac atttatagat 300

tcctaggaat atgccaaagc ttttcaaagc ctctatggac agctcatlcc ttaacttttc 360

ctcttttaaaa tcttttttan cttctttatt gccccagcca ctatcactgc ctccaggcagc 420

tgcaacglla aacaattgcc actgattact ttcaacaaat aacctcanag aaaaggctgt 480

gigtattgaa tgggtatcaa gtcacgic

508

&lt;210&gt; 133

&lt;211&gt; 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (313)

&lt;223&gt; a, c, g or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (336)

&lt;223&gt; g or c

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (401)

&lt;223&gt; g or c

&lt;400&gt; 133

gtcgactcga gcggccgcgg accgtttttt ttttttttct ctctcttgcc ccttctaata 60

tcttggagag ggaatggagac tgaagagtga gtttggtcct ccacttgatc caggttctta 120

ttttgtttt ctacttcaaa gcgagaactt ggtactgtga ctttgataag aattgacttc 180

aggcccagca agatccctca tgccigttaat cccagcactt tggggggcca aggcaggagg 240

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aaaataaaat tanciggggt tgaiggtgca calcastggt cctggctact cgggaggcca 360  
aggtagggagg aatgcctgag gatcggaggt caaggctgca sigagccaat attgtgccac 420  
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ccgc 484

<210> 134

<211> 605

<212> DNA

<213> Homo sapiens

<400> 134

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ggaatttgag ttctctctaa cccagcttac tggggacat agaaaaactc agtagaaata 180  
ccttgggtga tctgttgag ttaagtctg atctgaat taaactcagt aagccactat 240  
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caaattagtt cttttcccc cagaggggaa agtatgttc tgcaaatagt gttgtctta 360

WO 01/25427

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 tataggaatc ctgtagtgcc actagttaaa tgccgaattc tcatctggat gttaccaatca 480  
 aacatcaglia cacttgteat ttcacatgig tttaatgiga cagtttttca gtactgtatg 540  
 tgtaatttc tacttttttt aatatttaaa attgctttta aataaacata ttctcagttg 600  
 atccc 605

&lt;210&gt; 135

&lt;211&gt; 1786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2).. (151)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (689)

&lt;223&gt; g or a

&lt;400&gt; 135

g gca cga ggg tcc tct gca tgg ggt cag gtg ctt ctg tgc ttg ctg tcc 49

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1

5

10

15

tac ctc tct cca cag cag ggc tct caa aac cat ttt gat ccc cca ttg 97  
 Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu  
 20 25 30  
 gca gag ggt tcc cct ctt tac aga gtt cag tca tta aaa gca tgg atc 145  
 Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile  
 35 40 45  
 agc tgt taatctcatt ggaggaggga actgtttcct gcattcattc atctgggaac 201  
 Ser Cys  
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 ctctcttgagt agccacigtc tgccagccac tgcctciagag atgggaaaac agcacggaac 261  
 aaaaccaagg tcctttctec agcgaattta tatccttcag gaagctgggt cctgccacca 321  
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<210> 136

<211> 50

<212> PRT

<213> Homo sapiens

<400> 136

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1 5 10 15

Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

20 25 30

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

35 40 45

Ser Cys

50

<210> 137

<211> 835

<212> DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (535).. (729)

&lt;400&gt; 137

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 aatcagcctc atgactttat agttatgtct tgtattttaa aacatttttt atacatttgg 480  
 ttatgttgal aaaccaaaaa catttgatta ataaaatata tatttgaata aatt atg 537

Met

1

agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585

Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr

5

10

15

aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633

Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr

20

25

30

tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681

Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu

35

40

45

aga ttt tcc att aac tat ttt ttt caa aga ctc aaa ttt tgt acc aag 729

Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys

50 55 60 65

taaatccagg ctttatglac aaacatgttg ttgtttttat ttggggctgg gggaggtata 789

tgatgagcag acttcicgga attcataata aattttctaa aagcct 835

<210> 138

<211> 65

<212> PRT

<213> Homo sapiens

<400> 138

Met Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile

1 5 10 15

Tyr Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met

20 25 30

Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu

35 40 45

Leu Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr

50 55 60

Lys

65

<210> 139

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (201)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (348)

&lt;223&gt; t or c

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (353)

&lt;223&gt; a or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (358)

&lt;223&gt; a or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (363)

&lt;223&gt; a or t

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (368)

&lt;223&gt; g or a

&lt;400&gt; 139

tgt ttc agt gtg act gtc ttg tta gag gtg aag ttt atc cag ggt aac 48

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1

5

10

15

ttg ctc act aac tat tcc ttt tta tgg cct ggg gtt aaa ggg agc atg 96

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met  
                   20                  25                  30  
 gct cac act ggt gaa aat aag gaa ggc ctg gtc tta tct tgt att aat 144  
 Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn  
                   35                  40                  45  
 aat act ggc tgc att cca cca gcc aga gat ttc tat ctg cga aga cct 192  
 Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro  
                   50                  55                  60  
 atg aaa cac tgaagagaaa ttaggcaga aggaaatggc cacatacac 241  
 Met Lys His  
                   65  
 aagtictatt atatactctt ttgtaaatac atattgtata ttacttggat gttttcttat 301  
 atcatttact gtctttttga gttaatgtca gtttttactc tctcaaytta cwatgtwaca 361  
 twgtaartaa cataaigtcc ttattatatt atatttaagc atctaacata tagagtgtt 421  
 ttcatataag tttaagataa atgtcaaaaa tatatgttct ttgtttttc ttgctttta 481  
 aattatgtat cttttccttt tctttttttt aagaataatt tattgttcag gagaaagaat 541  
 gtatatgtaa ctgaaactat ctgaagaatg cacattgaag gccgtgaggt actgataaac 601  
 taaagaattt attattcaaa atact 626

&lt;210&gt; 140

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn  
           1                  5                  10                  15  
 Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

20 25 30  
 Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn  
 35 40 45  
 Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro  
 50 55 60  
 Met Lys His

65

&lt;210&gt; 141

&lt;211&gt; 525

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (103).. (525)

&lt;400&gt; 141

aagaaatgga ggactcagaa ccaaggattt ccaagigatt tcttccaaag cacaggaatc 60  
 tcactctgtt aaagctggtc tgttctaact gagatgacag tc atg tcc ctt tcc 114  
 Met Ser Leu Ser

1

agg gac ctc aag gac gac ttt cac agt gac acg gta ctc tcc atc tta 162  
 Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val Leu Ser Ile Leu  
 5 10 15 20  
 aat gag cag cgc att cgg ggc att tta tgc gat gtc act atc att gtg 210  
 Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val Thr Ile Ile Val  
 25 30 35  
 gaa gat acc aaa ttt aaa gcc cat agc aat gtt ctg gca gct tca agc 258

Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser  
                   40                  45                  50  
 ctg tat ttt aaa aat atc ttt tgg agc cat aca atc tgt att tcc agc 306  
 Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser  
                   55                  60                  65  
 cac gtc ctg gag ctg gac gat ctc aaa gct gaa gtg ttt act gaa ata 354  
 His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile  
                   70                  75                  80  
 ctt aat tat atc tac agt tcc aca gtc gtt gtc aag aga cag gaa aca 402  
 Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys Arg Gln Glu Thr  
                   85                  90                  95                  100  
 gtc act gat ctc gca gct gca gga aaa aag ctg gga ata tcg ttc ttg 450  
 Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly Ile Ser Phe Leu  
                   105                  110                  115  
 gaa gac ctt act gat cgc aac ttc tca aat tcc ccg ggt ccc tat gta 498  
 Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro Gly Pro Tyr Val  
                   120                  125                  130  
 ttc tgt att act gaa aag gga gtg gtt 525  
 Phe Cys Ile Thr Glu Lys Gly Val Val  
                   135                  140

&lt;210&gt; 142

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met Ser Leu Ser Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val

1 5 10 15  
Leu Ser Ile Leu Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val  
20 25 30  
Thr Ile Ile Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu  
35 40 45  
Ala Ala Ser Ser Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile  
50 55 60  
Cys Ile Ser Ser His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val  
65 70 75 80  
Phe Thr Glu Ile Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys  
85 90 95  
Arg Gln Glu Thr Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly  
100 105 110  
Ile Ser Phe Leu Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro  
115 120 125  
Gly Pro Tyr Val Phe Cys Ile Thr Glu Lys Gly Val Val  
130 135 140

&lt;210&gt; 143

&lt;211&gt; 1827

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (138).. (1307)

&lt;400&gt; 143

gagacttggg ctggagccgc cctgggtgtc agcggctcgg ctcccgcgca cgctccggcc 60



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gtcgcgcagc ctccggcacct gcaggcccggt gcgtcccgcg gctggcgccc ctgactccgt 120
cccggccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac 170
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn
1 5 10
ttg ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc tcg 218
Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser
15 20 25
cgg gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg 266
Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val
30 35 40
gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag 314
Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu
45 50 55
gtg tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc 362
Val Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
60 65 70 75
aaa cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc 410
Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val
80 85 90
aca aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg 458
Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg
95 100 105
aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc 506
Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro
110 115 120
tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc 554
Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly

```

125	130	135	
cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct	602		
His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro			
140	145	150	155
cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc	650		
Pro Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr			
160	165	170	
ctg agc tgc cag tct cca agg agt aag cct gct gtc caa tac cag tgg	698		
Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp			
175	180	185	
gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat	746		
Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp			
190	195	200	
gtc atc cgt ggg tct tta agc ctc acc aac ctt tgc tct tcc atg gct	794		
Val Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala			
205	210	215	
gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt	842		
Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys			
220	225	230	235
aat gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct	890		
Asn Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala			
240	245	250	
gga gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg	938		
Gly Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu			
255	260	265	
gtc ctc ttg tac cac cgc cgg ggc aag gcc ctg gag gag cca gcc aat	986		

Val Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn  
 270 275 280  
 gat atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag 1034  
 Asp Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys  
 285 290 295  
 agc tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc 1082  
 Ser Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser  
 300 305 310 315  
 gca cga gcc ctc tgg cca ccc cat ggc cct ccc agg cct ggt gca ttg 1130  
 Ala Arg Ala Leu Trp Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu  
 320 325 330  
 acc ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg 1178  
 Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu  
 335 340 345  
 ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt 1226  
 Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly  
 350 355 360  
 ggg gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg 1274  
 Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met  
 365 370 375  
 gtg cct gcc cag agt caa gct ggc tct ctg gta tgatgacccc accactcatt 1327  
 Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val  
 380 385 390  
 ggctaaagga ttgggggtct ctcttccta taagggtcac ctctagcaca gaggcctgag 1387  
 tcatgggaaa gagtcacact cctgaccctt agtactctgc cccaccctct ctttactgtg 1447  
 ggaaaaccaa ctcagtaaga cctaagtgtc caggagacag aaggagaaga ggaagtggat 1507  
 ctggaattgg gaggagcctc caccaccccc tgactcctcc ttatgaagcc agctgctgaa 1567

attagclact caccaagagi gaggggcaga gacliccagt cactgagtct cccaggcccc 1627  
 cttagatctgt accccacccc tatctaacac cacccttggc tcccactcca gctccctgta 1687  
 ttgatataac cgtcaggct ggcttggta gglttactg gggcagagga tagggaatct 1747  
 cttattaaaa ctaacatgaa atatgtgttg ttctatttg caaatltaaa taaagataca 1807  
 taatgttgt atgagataag 1827

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1 5 10 15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln

20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val

35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr  
 130 135 140  
 Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu  
 145 150 155 160  
 Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser  
 165 170 175  
 Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro  
 180 185 190  
 Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser  
 195 200 205  
 Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys  
 210 215 220  
 Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu  
 225 230 235 240  
 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly  
 245 250 255  
 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His  
 260 265 270  
 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp  
 275 280 285  
 Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300  
 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp  
 305 310 315 320  
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

340

345

350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

355

360

365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

370

375

380

Gln Ala Gly Ser Leu Val

385

390

&lt;210&gt; 145

&lt;211&gt; 3466

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (84).. (2726)

&lt;400&gt; 145

tgcgggaagc gatgtagtag ctgccaggct gtccccgcc ctgcccgcc cgagccccgc 60

gggccgccgc cgccaccgcc gcc atg aag aag cag ttc aac cgc atg aag cag 113

Met Lys Lys Gln Phe Asn Arg Met Lys Gln

1

5

10

ctg gct aac cag acc gtg ggc aga gct gag aaa aca gaa gtc ctt agt 161

Leu Ala Asn Gln Thr Val Gly Arg Ala Glu Lys Thr Glu Val Leu Ser

15

20

25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata 209

Glu Asp Leu Leu Gln Ile Glu Arg Arg Leu Asp Thr Val Arg Ser Ile

30

35

40

tgc cac cat tcc cat aag cgc ttg gtg gca tgt ttc cag ggc cag cat	257
Cys His His Ser His Lys Arg Leu Val Ala Cys Phe Gln Gly Gln His	
45 50 55	
ggc acc gat gcc gag agg aga cac aaa aaa ctg cct ctg aca gct ctt	305
Gly Thr Asp Ala Glu Arg Arg His Lys Lys Leu Pro Leu Thr Ala Leu	
60 65 70	
gct caa aat atg caa gaa gca tgc act cag ctg gaa gac tct ctc ctg	353
Ala Gln Asn Met Gln Glu Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu	
75 80 85 90	
ggg aag atg ctg gag acg tgt gga gat gct gag aat cag ctg gct ctc	401
Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu	
95 100 105	
gag ctc tcc cag cac gaa gtc ttt gtt gag aag gag atc gtg gac cct	449
Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro	
110 115 120	
ctg tac ggc ata gct gag gtg gag att ccc aac atc cag aag cag agg	497
Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg	
125 130 135	
aag cag ctt gca aga ttg gtg tta gac tgg gat tca gtc aga gcc agg	545
Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg	
140 145 150	
tgg aac caa gct cac aaa tcc tca gga acc aac ttt cag ggc ctt cca	593
Trp Asn Gln Ala His Lys Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro	
155 160 165 170	
tca aaa ata gat act cta aag gaa gag atg gat gaa gct gga aat aaa	641
Ser Lys Ile Asp Thr Leu Lys Glu Glu Met Asp Glu Ala Gly Asn Lys	
175 180 185	

gta gaa cag tgc aag gat caa ctt gca gca gac atg tac aac ttt atg 689  
 Val Glu Gln Cys Lys Asp Gln Leu Ala Ala Asp Met Tyr Asn Phe Met  
 190 195 200  
 gcc aaa gaa ggg gag tat ggc aaa ttc ttt gtt acg tta tta gaa gcc 737  
 Ala Lys Glu Gly Glu Tyr Gly Lys Phe Phe Val Thr Leu Leu Glu Ala  
 205 210 215  
 caa gca gat tac cat aga aaa gca tta gca gtc tta gaa aag acc ctc 785  
 Gln Ala Asp Tyr His Arg Lys Ala Leu Ala Val Leu Glu Lys Thr Leu  
 220 225 230  
 ccc gaa atg cga gcc cat caa gat aag tgg gcg gaa aaa cca gcc ttt 833  
 Pro Glu Met Arg Ala His Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe  
 235 240 245 250  
 ggg act ccc cta gaa gaa cac ctg aag agg agc ggg cgc gag att gcg 881  
 Gly Thr Pro Leu Glu Glu His Leu Lys Arg Ser Gly Arg Glu Ile Ala  
 255 260 265  
 ctg ccc att gaa gcc tgt gtc atg ctg ctt ctg gag aca ggc atg aag 929  
 Leu Pro Ile Glu Ala Cys Val Met Leu Leu Leu Glu Thr Gly Met Lys  
 270 275 280  
 gag gag ggc ctt ttc cga att ggg gct ggg gcc tcc aag tta aag aag 977  
 Glu Glu Gly Leu Phe Arg Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys  
 285 290 295  
 ctg aaa gct gct ttg gac tgt tct act tct cac ctg gat gag ttc tat 1025  
 Leu Lys Ala Ala Leu Asp Cys Ser Thr Ser His Leu Asp Glu Phe Tyr  
 300 305 310  
 tca gac ccc cat gct gta gca ggt gct tta aaa tcc tat tta cgg gaa 1073  
 Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu



315	320	325	330	
ttg cct gaa cct ttg atg act ttt aat ctg tat gaa gaa tgg aca caa	1121			
Leu Pro Glu Pro Leu Met Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln				
335	340	345		
gtt gca agt gtg cag gat caa gac aaa aaa ctt caa gac ttg tgg aga	1169			
Val Ala Ser Val Gln Asp Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg				
350	355	360		
aca tgt cag aag ttg cca cca caa aat ttt gtt aac ttt aga tat ttg	1217			
Thr Cys Gln Lys Leu Pro Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu				
365	370	375		
atc aag ttc ctt gca aag ctt gct cag acc agc gat gtg aat aaa atg	1265			
Ile Lys Phe Leu Ala Lys Leu Ala Gln Thr Ser Asp Val Asn Lys Met				
380	385	390		
act ccc agc aac att gcg att gtg tta ggc cct aac ttg tta tgg gcc	1313			
Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Ala				
395	400	405	410	
aga aat gaa gga aca ctt gct gaa atg gca gca gcc aca tcc gtc cat	1361			
Arg Asn Glu Gly Thr Leu Ala Glu Met Ala Ala Ala Thr Ser Val His				
415	420	425		
gtg gtt gca gtg att gaa ccc atc att cag cat gcc gac tgg ttc ttc	1409			
Val Val Ala Val Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe				
430	435	440		
cct gaa gag gtg gaa ttt aat gta tca gaa gca ttt gta cct ctc acc	1457			
Pro Glu Glu Val Glu Phe Asn Val Ser Glu Ala Phe Val Pro Leu Thr				
445	450	455		
acc ccg agt tct aat cac tca ttc cac act gga aac gac tct gac tcg	1505			
Thr Pro Ser Ser Asn His Ser Phe His Thr Gly Asn Asp Ser Asp Ser				

460	465	470	
ggg acc ctg gag agg aag cgg cct gct agc atg gcg gtg atg gaa gga	1553		
Gly Thr Leu Glu Arg Lys Arg Pro Ala Ser Met Ala Val Met Glu Gly			
475	480	485	490
gac ttg gtg aag aag gaa agc ttt ggt gtg aag ctt atg gac ttc cag	1601		
Asp Leu Val Lys Lys Glu Ser Phe Gly Val Lys Leu Met Asp Phe Gln			
495	500	505	
gcc cac cgg cgg ggt ggc act cta aat aga aag cac ata tcc ccc gct	1649		
Ala His Arg Arg Gly Gly Thr Leu Asn Arg Lys His Ile Ser Pro Ala			
510	515	520	
ttc cag ccg cca ctt ccg ccc aca gat ggc agc acc gtg gtg ccc gct	1697		
Phe Gln Pro Pro Leu Pro Pro Thr Asp Gly Ser Thr Val Val Pro Ala			
525	530	535	
ggc cca gag ccc cct ccc cag agc tct agg gct gaa agc agc tct ggg	1745		
Gly Pro Glu Pro Pro Pro Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly			
540	545	550	
ggt ggg act gtc ccc tct tcc gcg ggc ata ctg gag cag ggg ccg agc	1793		
Gly Gly Thr Val Pro Ser Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser			
555	560	565	570
cca ggc gac ggc agt cct ccc aaa ccg aag gac cct gla tct gca gct	1841		
Pro Gly Asp Gly Ser Pro Pro Lys Pro Lys Asp Pro Val Ser Ala Ala			
575	580	585	
gtg cca gca cca ggg aga aac aac agt cag ata gca tct ggc caa aat	1889		
Val Pro Ala Pro Gly Arg Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn			
590	595	600	
cag ccc cag gca gct gct ggc tcc cac cag ctc tcc atg ggc caa cct	1937		

Gln Pro Gln Ala Ala Ala Gly Ser His Gln Leu Ser Met Gly Gln Pro  
 605 610 615  
 cac aat gct gca ggg ccc agc ccg cat aca ctg cgc cga gct gtt aaa 1985  
 His Asn Ala Ala Gly Pro Ser Pro His Thr Leu Arg Arg Ala Val Lys  
 620 625 630  
 aaa ccc gct cca gca ccc ccg aaa ccg ggc aac cca cct cct ggc cac 2033  
 Lys Pro Ala Pro Ala Pro Pro Lys Pro Gly Asn Pro Pro Pro Gly His  
 635 640 645 650  
 ccc ggg ggc cag agt tct tca gga aca tct cag cat cca ccc agt ctg 2081  
 Pro Gly Gly Gln Ser Ser Ser Gly Thr Ser Gln His Pro Pro Ser Leu  
 655 660 665  
 tca cca aag cca ccc acc cga agc ccc tct cct ccc acc cag cac acg 2129  
 Ser Pro Lys Pro Pro Thr Arg Ser Pro Ser Pro Pro Thr Gln His Thr  
 670 675 680  
 ggc cag cct cca ggc cag ccc tcc gcc ccc tcc cag ctc tca gca ccc 2177  
 Gly Gln Pro Pro Gly Gln Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro  
 685 690 695  
 cgg agg tac tcc agc agc ttg tct cca atc caa gct ccc aat cac cca 2225  
 Arg Arg Tyr Ser Ser Ser Leu Ser Pro Ile Gln Ala Pro Asn His Pro  
 700 705 710  
 ccg ccg cag ccc cct acg cag gcc acg cca ctg atg cac acc aaa ccc 2273  
 Pro Pro Gln Pro Pro Thr Gln Ala Thr Pro Leu Met His Thr Lys Pro  
 715 720 725 730  
 aat agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga 2321  
 Asn Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly  
 735 740 745  
 ctt gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt 2369

Leu Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser  
                   750                          755                          760  
 act ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc 2417  
 Thr Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr  
                   765                          770                          775  
 ctg gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta 2465  
 Leu Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu  
                   780                          785                          790  
 ccg aga ccg aga cca gta cca aag cca agg aac cgg ccc agc gtg ccc 2513  
 Pro Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro  
 795                          800                          805                          810  
 cca ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc 2561  
 Pro Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu  
                           815                          820                          825  
 acc aac aca gca cca aca gct tcc aag ata gta aca gac tcc aat tcc 2609  
 Thr Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser  
                   830                          835                          840  
 agg gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac 2657  
 Arg Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp  
                   845                          850                          855  
 tca gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat 2705  
 Ser Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn  
                   860                          865                          870  
 gat acc gag agc act gcc ctg tgaagaaagc cctttccag ccctccacca 2756  
 Asp Thr Glu Ser Thr Ala Leu  
 875                          880

ctccaccct ggcgagtga gcaggggcag gcgaacctct ttccttgag accgaacagt 2816  
 gaaaagcttt cagtgagga caaaggagg cctcactgig cgggacctgg ccttctgcac 2876  
 ggccaagga gaacctggag gccaccacta aagctgaatg acctgtgtct tgaagaagtt 2936  
 ggctttcttt acatgggaag gaaatcatgc caaaaaaalc caaaacaaag aagtacctgg 2996  
 agtggagaga glattcctgc tgaaacgcgc ataggaagct ttgtccctg ctgttaatgc 3056  
 gggcagcacc tacagcaact tggaatgagt aagaagcagt gcgttaacta tctatttaal 3116  
 aaaaatgcgt cattatgcaa gtcgcctact ctctgtacc tggacgttca ttcttatgta 3176  
 ttaggaggga ggctgcgtc cttcagactt gctgcagaat cattttgtat catgtatggt 3236  
 ctgtgtctcc ccagtcacct cagaacctatg cccatggatg gtgactgcig gctctgtcac 3296  
 ctcatcaaac tggatgtgac ccatgccgcc tcgttggatt gtcggaatgt agacagaaat 3356  
 gtactgttct ttttttttt tttaaacaat gtaattgcta ctgtataagg accgaacatt 3416  
 attctagttt catgtttaal ttgaattaaa tatattctgt ggtttataig 3466

<210> 146

<211> 881

<212> PRT

<213> Homo sapiens

<400> 146

Met Lys Lys Gln Phe Asn Arg Met Lys Gln Leu Ala Asn Gln Thr Val

1 5 10 15

Gly Arg Ala Glu Lys Thr Glu Val Leu Ser Glu Asp Leu Leu Gln Ile

20 25 30

Glu Arg Arg Leu Asp Thr Val Arg Ser Ile Cys His His Ser His Lys

35 40 45

Arg Leu Val Ala Cys Phe Gln Gly Gln His Gly Thr Asp Ala Glu Arg

50 55 60

Arg His Lys Lys Leu Pro Leu Thr Ala Leu Ala Gln Asn Met Gln Glu

65	70	75	80
Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu Gly Lys Met Leu Glu Thr			
85	90	95	
Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu Glu Leu Ser Gln His Glu			
100	105	110	
Val Phe Val Glu Lys Glu Ile Val Asp Pro Leu Tyr Gly Ile Ala Glu			
115	120	125	
Val Glu Ile Pro Asn Ile Gln Lys Gln Arg Lys Gln Leu Ala Arg Leu			
130	135	140	
Val Leu Asp Trp Asp Ser Val Arg Ala Arg Trp Asn Gln Ala His Lys			
145	150	155	160
Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro Ser Lys Ile Asp Thr Leu			
165	170	175	
Lys Glu Glu Met Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp			
180	185	190	
Gln Leu Ala Ala Asp Met Tyr Asn Phe Met Ala Lys Glu Gly Glu Tyr			
195	200	205	
Gly Lys Phe Phe Val Thr Leu Leu Glu Ala Gln Ala Asp Tyr His Arg			
210	215	220	
Lys Ala Leu Ala Val Leu Glu Lys Thr Leu Pro Glu Met Arg Ala His			
225	230	235	240
Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe Gly Thr Pro Leu Glu Glu			
245	250	255	
His Leu Lys Arg Ser Gly Arg Glu Ile Ala Leu Pro Ile Glu Ala Cys			
260	265	270	
Val Met Leu Leu Leu Glu Thr Gly Met Lys Glu Glu Gly Leu Phe Arg			
275	280	285	

Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys Leu Lys Ala Ala Leu Asp  
 290 295 300  
 Cys Ser Thr Ser His Leu Asp Glu Phe Tyr Ser Asp Pro His Ala Val  
 305 310 315 320  
 Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro Leu Met  
 325 330 335  
 Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln Val Ala Ser Val Gln Asp  
 340 345 350  
 Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg Thr Cys Gln Lys Leu Pro  
 355 360 365  
 Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu Ile Lys Phe Leu Ala Lys  
 370 375 380  
 Leu Ala Gln Thr Ser Asp Val Asn Lys Met Thr Pro Ser Asn Ile Ala  
 385 390 395 400  
 Ile Val Leu Gly Pro Asn Leu Leu Trp Ala Arg Asn Glu Gly Thr Leu  
 405 410 415  
 Ala Glu Met Ala Ala Ala Thr Ser Val His Val Val Ala Val Ile Glu  
 420 425 430  
 Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Glu Glu Val Glu Phe  
 435 440 445  
 Asn Val Ser Glu Ala Phe Val Pro Leu Thr Thr Pro Ser Ser Asn His  
 450 455 460  
 Ser Phe His Thr Gly Asn Asp Ser Asp Ser Gly Thr Leu Glu Arg Lys  
 465 470 475 480  
 Arg Pro Ala Ser Met Ala Val Met Glu Gly Asp Leu Val Lys Lys Glu  
 485 490 495

Ser Phe Gly Val Lys Leu Met Asp Phe Gln Ala His Arg Arg Gly Gly  
 500 505 510  
 Thr Leu Asn Arg Lys His Ile Ser Pro Ala Phe Gln Pro Pro Leu Pro  
 515 520 525  
 Pro Thr Asp Gly Ser Thr Val Val Pro Ala Gly Pro Glu Pro Pro Pro  
 530 535 540  
 Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly Gly Gly Thr Val Pro Ser  
 545 550 555 560  
 Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser Pro Gly Asp Gly Ser Pro  
 565 570 575  
 Pro Lys Pro Lys Asp Pro Val Ser Ala Ala Val Pro Ala Pro Gly Arg  
 580 585 590  
 Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn Gln Pro Gln Ala Ala Ala  
 595 600 605  
 Gly Ser His Gln Leu Ser Met Gly Gln Pro His Asn Ala Ala Gly Pro  
 610 615 620  
 Ser Pro His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro  
 625 630 635 640  
 Pro Lys Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser  
 645 650 655  
 Ser Gly Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr  
 660 665 670  
 Arg Ser Pro Ser Pro Pro Thr Gln His Thr Gly Gln Pro Pro Gly Gln  
 675 680 685  
 Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro Arg Arg Tyr Ser Ser Ser  
 690 695 700  
 Leu Ser Pro Ile Gln Ala Pro Asn His Pro Pro Pro Gln Pro Pro Thr



705                      710                      715                      720  
 Gln Ala Thr Pro Leu Met His Thr Lys Pro Asn Ser Gln Gly Pro Pro  
                          725                      730                      735  
 Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu Glu Gln Pro Ser His  
                          740                      745                      750  
 Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr Pro Pro Leu Gly Lys  
                          755                      760                      765  
 Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu Ala Gly Gly Asn Pro  
                          770                      775                      780  
 Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro Arg Pro Arg Pro Val  
 785                      790                      795                      800  
 Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro Pro Pro Gln Pro Pro  
                          805                      810                      815  
 Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr Asn Thr Ala Pro Thr  
                          820                      825                      830  
 Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg Val Ser Glu Pro His  
                          835                      840                      845  
 Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser Ala Ser Lys Asp Val  
                          850                      855                      860  
 Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp Thr Glu Ser Thr Ala  
 865                      870                      875                      880  
 Leu

&lt;210&gt; 147

&lt;211&gt; 3021

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (140).. (1105)

&lt;400&gt; 147

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acagccigtgtt ccaagtgtgg cttaatccgt ctccaccacc agatctttct ccgtggattc 120
ctctgciaag accgcigcc atg cca gtg acg gta acc cgc acc acc atc aca 172

      Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr
              1              5              10
acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg atc gtg ggg 220
Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly
              15              20              25
tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag 268
Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln
              30              35              40
ctg gtg tct acc tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc gcc 316
Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala
              45              50              55
tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc 364
Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
              60              65              70              75
ttc tcc gtg acc ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag 412
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln
              80              85              90
gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc 460
Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys

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95	100	105	
tat gcg ggc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc	508		
Tyr Ala Gly Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr			
110	115	120	
tat gtc cag ttc ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc	556		
Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala			
125	130	135	
gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg	604		
Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val			
140	145	150	155
gcc tgg acc cgg gcc cgg ccc ggc gag atc act ggc tat atg gcc acc	652		
Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr			
160	165	170	
gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc	700		
Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile			
175	180	185	
ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg gcc ctg	748		
Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu			
190	195	200	
gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc	796		
Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile			
205	210	215	
gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtc cta ccc atc ccc	844		
Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro			
220	225	230	235
ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat	892		
Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr			

240 245 250  
 gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat 940  
 Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr  
 255 260 265  
 ggc ggc cag cct cgg cgc tcg aga gat gla agc tgc agc cgc agc cat 988  
 Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His  
 270 275 280  
 gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg 1036  
 Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu  
 285 290 295  
 acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc 1084  
 Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala  
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 cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct cccgttccct 1135  
 His Leu Val Phe Val Lys Val  
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 ttctttttaa tatcaatata aaagg 3021

&lt;210&gt; 148

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr Ser

1

5

10

15

Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu

20

25

30

Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys

35

40

45

Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met

50

55

60

Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu

65

70

75

80

Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu

85

90

95

Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Gly Leu Phe

100

105

110

Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu

115

120

125

Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser

130

135

140

Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala

145

150

155

160

Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu

165

170

175

Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser

180

185

190

Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala

195

200

205

Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn

210 215 220

Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu

225 230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val

245 250 255

Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg

260 265 270

Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys

275 280 285

Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu

290 295 300

Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val

305 310 315 320

Lys Val

<210> 149

<211> 4409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (39).. (2027)

<400> 149

gggtgcagga tcgcagaaag tatgtccctt ctctcacc atg agc tgg ctc tcc agt 56

Met Ser Trp Leu Ser Ser

1

5

tcc cag gga gtg gta cta aca gcc tac cac ccc agc ggc aag gac cag 104  
 Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln  
                   10                  15                  20  
 gcc gtc ggg aac agc cat gca aag gca ggg gag gaa gcc acc tcg agt 152  
 Ala Val Gly Asn Ser His Ala Lys Ala Gly Glu Glu Ala Thr Ser Ser  
                   25                  30                  35  
 cgc aga tat ggc cag tac act atg aac cag gaa agc acc acc atc aaa 200  
 Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln Glu Ser Thr Thr Ile Lys  
                   40                  45                  50  
 gtt atg gag aag cct cca ttt gat cga tca att tcc cag gat tct ttg 248  
 Val Met Glu Lys Pro Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu  
                   55                  60                  65                  70  
 gat gaa cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc aag 296  
 Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys  
                   75                  80                  85  
 aaa tct agt gaa aac agc caa gaa gat caa gag gtg gtt gtt gtc aaa 344  
 Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys  
                   90                  95                  100  
 gag cct gat gag gga gaa ttg gaa gaa gag tgg ctt aaa gag gcc ggt 392  
 Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu Trp Leu Lys Glu Ala Gly  
                   105                  110                  115  
 tta tcc aat ctc ttc gga gag tct gct gga gat cca cag gaa agc att 440  
 Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile  
                   120                  125                  130  
 gtg ttt tta tca aca ttg acg cgg acc cag gca gca gca gtt cag aag 488  
 Val Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys



135	140	145	150	
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac aaa cag tac	536			
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln Tyr				
155	160	165		
cag att cct gac gtc aga gac ata ttt gct caa cag aga gaa tca aaa	584			
Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu Ser Lys				
170	175	180		
gaa aca gct cca ggt ggc act gaa tgc cag tca ctt aga aca aat gaa	632			
Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg Thr Asn Glu				
185	190	195		
aac aaa tac caa gga aga gat gac gag gca tct aac ctt gtt ggt gaa	680			
Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu				
200	205	210		
gag aag ctg atc cca cct gag gag acg cct gcc cct gaa aca gac atc	728			
Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr Asp Ile				
215	220	225	230	
aac ctg gag gta tca ttt gcc gag caa gca ctc aat cag aaa gag agc	776			
Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu Asn Gln Lys Glu Ser				
235	240	245		
tcc aag gag aaa atc cag aag agc aaa ggc gat gat gcc aca tta cct	824			
Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly Asp Asp Ala Thr Leu Pro				
250	255	260		
agt ttc aga ttg cca aaa gac aaa acg ggt acc aca agg att ggt gac	872			
Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp				
265	270	275		
ctc gca ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att gag	920			
Leu Ala Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile Glu				

280	285	290	
ctg act gcc ctc tat gat gta ttg ggt att gag ctg aaa caa caa aaa	968		
Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu Lys Gln Gln Lys			
295	300	305	310
gct gtg aaa atc aaa aca aaa gat tct ggt ctt ttt tgc gtt cca ttg	1016		
Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu			
315	320	325	
aca gcg cta tta gaa caa gat cag agg aaa gta cca gga atg cga ata	1064		
Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile			
330	335	340	
ccc ttg atc ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg	1112		
Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu			
345	350	355	
gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att aga atc aag	1160		
Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys			
360	365	370	
aat ctt tgc caa gaa cta gaa gca aag ttt tat gaa ggg act ttt aat	1208		
Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn			
375	380	385	390
tgg gaa agt gtc aaa cag cat gat gcc gcc agc ctg ctg aag ctc ttc	1256		
Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu Phe			
395	400	405	
att cgg gag ttg ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc	1304		
Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala			
410	415	420	
ttt cag gct gtc cag aat ctt cca acc aag aag cag caa cta cag gct	1352		

Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu Gln Ala  
 425 430 435  
 ttg aac ctt ctt ggc atc ctc cta cct gat gca aac agg gac aca ctg 1400  
 Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp Ala Asn Arg Asp Thr Leu  
 440 445 450  
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 Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile Asp Asn Lys Glu Lys  
 455 460 465 470  
 aat aaa atg aca gtc atg aat gta gca atg gtc atg gcc ccg aat ctc 1496  
 Asn Lys Met Thr Val Met Asn Val Ala Met Val Met Ala Pro Asn Leu  
 475 480 485  
 ttt atg tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa ttt 1544  
 Phe Met Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu Phe  
 490 495 500  
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35 40 45

Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser

50 55 60

Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile

65 70 75 80

Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln

85 90 95

Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu

100 105 110

Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly

115 120 125

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                          595                      600                      605  
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                          610                      615                      620  
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 625                      630                      635                      640  
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 Val Ile Lys Ser Lys Pro Leu  
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Ser Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe
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Ala Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg
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 gtaccaacc agactttaaa taaaacaaac atgaaacct 4490

<210> 152

<211> 863

<212> PRT

<213> Homo sapiens

<400> 152

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Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser Pro

20 25 30

Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp Asp

35 40 45

Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn Gly

50 55 60

Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro Ser

65 70 75 80

Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe Asp

85 90 95

Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn Ser

100 105 110

Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His Ala

115 120 125  
Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg Ser  
130 135 140  
Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala Pro  
145 150 155 160  
Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu Gln  
165 170 175  
Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg Lys  
180 185 190  
Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro Gly  
195 200 205  
Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu Asp  
210 215 220  
Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile His  
225 230 235 240  
Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser Met  
245 250 255  
Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser Cys  
260 265 270  
Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val Lys  
275 280 285  
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp  
290 295 300  
Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser  
305 310 315 320  
Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp  
325 330 335

Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala  
 340 345 350  
 Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp  
 355 360 365  
 Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His Ile  
 370 375 380  
 His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala  
 385 390 395 400  
 Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro  
 405 410 415  
 Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser  
 420 425 430  
 Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr  
 435 440 445  
 Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu  
 450 455 460  
 Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn  
 465 470 475 480  
 Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp  
 485 490 495  
 Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro  
 500 505 510  
 Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys  
 515 520 525  
 Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys  
 530 535 540

Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys  
 545                      550                      555                      560  
 Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu  
                          565                      570                      575  
 Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg  
                          580                      585                      590  
 Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr Gln  
                          595                      600                      605  
 Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg  
                          610                      615                      620  
 Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val Leu  
 625                      630                      635                      640  
 Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala  
                          645                      650                      655  
 Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe  
                          660                      665                      670  
 Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg  
                          675                      680                      685  
 Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys  
                          690                      695                      700  
 Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe  
 705                      710                      715                      720  
 Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu  
                          725                      730                      735  
 Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu  
                          740                      745                      750  
 Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val Ser

755	760	765	
Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn Gly			
770	775	780	
Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu Leu			
785	790	795	800
Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu			
	805	810	815
Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp			
	820	825	830
Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu			
	835	840	845
Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile			
850	855	860	

&lt;210&gt; 153

&lt;211&gt; 2194

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (133).. (1125)

&lt;400&gt; 153

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gcggggcgccg gc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc cct 171

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro

1

5

10

ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg gtc 219  
 Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val  
 15 20 25  
 aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc ttc 267  
 Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe  
 30 35 40 45  
 agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag ccc 315  
 Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro  
 50 55 60  
 cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac gcg 363  
 Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala  
 65 70 75  
 ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga gca 411  
 Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala  
 80 85 90  
 aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct gtc 459  
 Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val  
 95 100 105  
 tta atg cac gat aac aca gla gat agg acg act gat ggg act ggg cga 507  
 Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg  
 110 115 120 125  
 ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca gca 555  
 Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala  
 130 135 140  
 aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc cta 603  
 Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu

145	150	155	
agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc ttt			651
Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe			
160	165	170	
gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa atg			699
Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met			
175	180	185	
tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct ttc			747
Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe			
190	195	200	205
ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata			795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile			
210	215	220	
aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg			843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly			
225	230	235	
aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg			891
Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met			
240	245	250	
gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg tgt			939
Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys			
255	260	265	
gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc tac			987
Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr			
270	275	280	285
ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act gtt			1035
Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val			

290	295	300	
aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc agc			1083
Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser			
305	310	315	
tat aic act gac agc atg gta gaa gac tgc gaa cct cac ttc			1125
Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe			
320	325	330	
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tcaaaatacc ctttgtgcta gcccaggccc tggggaatca ggtgactcac acaaatgcaa			1245
tagttggica ctgcattttt acctgaacca aagctaaacc cggtgttgcc accatgcacc			1305
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aggaggttga ggtgggagga tcacttgagc ccagaagttc aaggctgcaa tgagccatga			2145
ttacaccacg gcactacaac cttaggtggca cagtgagaac ctgactctt			2194

&lt;210&gt; 154



&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 154

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Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys

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Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu

35 40 45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg

50 55 60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn

65 70 75 80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val

85 90 95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His

100 105 110

Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp

115 120 125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg

130 135 140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala

145 150 155 160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys

165 170 175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu

180

185

190

Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu

195

200

205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

210

215

220

Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg

225

230

235

240

Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu

245

250

255

Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser

260

265

270

Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys

275

280

285

Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe

290

295

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305

310

315

320

Asp Ser Met Val Glu Asp Cys Glu Pro His Phe

325

330

<210> 155

<211> 3377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

&lt;222&gt; (44).. (1666)

&lt;400&gt; 155

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                                     1
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Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp Asp Ala Met Glu
   5             10             15             20
agc agc aag cct ggt cca gtg cag gtt gtt ttg gtt cag aaa gat caa    151
Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val Gln Lys Asp Gln
           25             30             35
cat tcc ttt gag cta gat gag aaa gcc ttg gcc agc atc ctc ttg cag    199
His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser Ile Leu Leu Gln
           40             45             50
gac cac atc cga gat ctt gat gtg gtg gtg gtt tca gtg gct ggt gcc    247
Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser Val Ala Gly Ala
           55             60             65
ttc cga aag ggc aag tcc ttc att ctg gat ttt atg cta cga tac tta    295
Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu
           70             75             80
tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa    343
Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu
           85             90             95             100
gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc    391
Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr
           105             110             115
act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt    439

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Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val Glu Lys Pro Gly  
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 Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln Gly Ala Phe Asp  
 135 140 145  
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 Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr  
 150 155 160  
 atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa 583  
 Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu  
 165 170 175 180  
 gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca 631  
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 200 205 210  
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 215 220 225  
 atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa 775  
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 230 235 240  
 gaa att cag aat gtt cga aat cac att cac tca tgt ttc tcc gat gtc 823  
 Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys Phe Ser Asp Val  
 245 250 255 260

acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct 871  
 Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro  
 265 270 275

gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag 919  
 Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln  
 280 285 290

tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa 967  
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 310 315 320

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 Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Ala  
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gcc tct gcc aag gac att tat tat aac aac atg gaa gag gtt tgt ggg 1159  
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 Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu Glu Lys His Cys  
 375 380 385

gaa ttc aaa caa ctt gct ctg gac cat ttt aag aag acc aag aag atg 1255  
 Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys Thr Lys Lys Met  
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 Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn Gly Ser Lys Asn  
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 His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp Ala Val Val Gly  
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 Arg Pro Ser Met Asp Lys Lys Ala Gln

535

540

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<210> 156

<211> 541

<212> PRT

<213> Homo sapiens

<400> 156

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 20 25 30  
 Gln Lys Asp Gln His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser  
 35 40 45  
 Ile Leu Leu Gln Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser  
 50 55 60  
 Val Ala Gly Ala Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met  
 65 70 75 80  
 Leu Arg Tyr Leu Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu  
 85 90 95  
 Gly Asp Pro Glu Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser  
 100 105 110  
 Asp Pro Glu Thr Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val  
 115 120 125  
 Glu Lys Pro Gly Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln  
 130 135 140



Gly Ala Phe Asp Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe  
145 150 155 160  
Ala Leu Ser Thr Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln  
165 170 175  
Asn Ile Gln Glu Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr  
180 185 190  
Gly Arg Leu Ala Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu  
195 200 205  
Met Phe Leu Val Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly  
210 215 220  
Leu Gln Gly Gly Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu  
225 230 235 240  
His Gln His Glu Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys  
245 250 255  
Phe Ser Asp Val Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val  
260 265 270  
Ala Thr Ser Pro Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu  
275 280 285  
Phe Lys Glu Gln Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser  
290 295 300  
Lys Leu Met Glu Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly  
305 310 315 320  
Leu Leu Glu Tyr Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp  
325 330 335  
Leu Pro His Pro Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn  
340 345 350

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Leu Ala Ala Ala Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu  
 355 360 365  
 Glu Val Cys Gly Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu  
 370 375 380  
 Glu Lys His Cys Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys  
 385 390 395 400  
 Thr Lys Lys Met Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu  
 405 410 415  
 Leu Glu Glu Glu Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn  
 420 425 430  
 Gly Ser Lys Asn Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe  
 435 440 445  
 Thr Gly Ile Val Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile  
 450 455 460  
 Gly Leu Glu Val Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu  
 465 470 475 480  
 Leu Ile Ala Leu Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr  
 485 490 495  
 Arg Glu Leu Gly Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu  
 500 505 510  
 Gln Ala Ser Ser His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp  
 515 520 525  
 Ala Val Val Gly Arg Pro Ser Met Asp Lys Lys Ala Gln  
 530 535 540

&lt;210&gt; 157

&lt;211&gt; 2172

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (45).. (563)

&lt;400&gt; 157

ggaacacggc acccgcacig cgcgicacgg igcaggccig gtat atg gac gac gcc 56

Met Asp Asp Ala

1

ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg 104

Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val

5

10

15

20

ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat 152

Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp

25

30

35

gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag 200

Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu

40

45

50

agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta 248

Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu

55

60

65

cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac 296

Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His

70

75

80

ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat 344

Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp

85

90

95

100

gig agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga 392

Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly

105

110

115

gac atg gig acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac 440

Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp

120

125

130

gag aag aac tac acg aag gcc atg cgg ctg ttt gig gga gaa ccg gig 488

Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val

135

140

145

tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag 536

Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln

150

155

160

tac gig aaa ttt ctg gca cag acc gcc tagcagtgtt gccctgggaac 583

Tyr Val Lys Phe Leu Ala Gln Thr Ala

165

170

taacacgtgc ctgtaaaagg tcccaaatgt aatgactgag cagaaaaatca atcacattct 643

ctttgctttt agaggatagc cttagaggcta gattatcttt cctttglaag attatttgat 703

cagaatattt tgaatgaaa ggatctagaa agcaacttgg aagtglaaag agtcaccttc 763

atittctgta actcaatcaa gactgggtggg tccatggccc tgtgttagtt catgattca 823

gttaggtccc aatgaaagt ttcattctcc gaaatgcagt tccttagatg cccatctgga 883

cgtgatgccg cgccgccgt gtaagaaggt gcaatcctag ataacacagc tagccagata 943

gaagacactt tttctccaa aatgatgcct tgggggtggg agtggtaggg ggaagagctc 1003

ccaccctaag gggcacacac tgagttgctt atgccacttc ctgttcaaa ataaagtaac 1063

tgccttaatc ttatactcat ggcttggagt taccttatat tcaggtatat gtgatatttt 1123

gccigtgttg ttaaaattgc cccatttaga ttctttctat aattgttctt atagataagt 1183

aatittatata tgagctgtgt tagtattttt tcagtgtgag atctctggat tctttcacia 1243

taaagctggt gaattttaac aggagiatta gtacataaat ttictactca acaattccga 1303  
 gataggatta tgcctagttt gtcataacac agaaaaactc caagttaact tcatgttttg 1363  
 gaagggcagg tcgtttttta agtattttct tttttaactg gatgaaaaat cticatgtta 1423  
 ggattaattt tcttaatcac ctccacactg tacagaggaa actcaagcct taaatgttta 1483  
 agtaaactct gctcagttt taggattaaa ataccacccg gtgggtgat gatgccatat 1543  
 accgcagggc ttgcttctgt caagtgtgac tctatctcag taattaaaaat aagtgcgat 1603  
 ctactgattt tttttaatgg atcatattct aaatgggcat tataaataga gcttgltcat 1663  
 ttttaagaac gaaacattca tatgataaac tategcttta aatlgccttt ctgcttcat 1723  
 ataacttttc cctgtcagga tcttagtgt ttgaaactcc tcgtgcgggg ctggcctcct 1783  
 gcggactcta gtctgcctc ctgatgtgg cgccgtggat ttcttcactt cagagctgta 1843  
 ttttacagg caagagtaag ttccgtggca cagtggctca tgcctgtaat ctacgtact 1903  
 caggaggcta aggtgggagg attcttagag ccgtggaggt cgaggctgca gtgagctgtg 1963  
 attgtggcca ctgcacacca gccgtgggtga cagagcgaga ctctgtctca aaaaagaaga 2023  
 aagagtaaga gctgaggcat ataataaat tctgtctaaag cacttaaggt gaaatcacat 2083  
 ttcttttcc caggatgttg ctacatctt tcgtttttat tgagggtgca tttatgtaca 2143  
 ataaaatgta ctcattttca gtgtttttg 2172

<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro

1 5 10 15

Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr

20 25 30

Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys

35 40 45  
Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys  
50 55 60  
Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu  
65 70 75 80  
Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser  
85 90 95  
Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe  
100 105 110  
Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg  
115 120 125  
Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val  
130 135 140  
Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu  
145 150 155 160  
Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala  
165 170

<210> 159

<211> 20

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 159

ggaagtgtta ctctgctct

20

<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 160

gagagagaga gagagagaga actagtcicg agtttttttt tttttttttt 50

<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt cccccccccc c 41

<210> 162

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence

<400> 162

agcaucgagu cggccuuguu ggccuacugg 30

<210> 163

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo(dT) primer sequence

<400> 163

gcggctgaag acggcctatg tggccttttt tttttttttt tt 42

<210> 164  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of the artificial sequence: an artificially synthesized primer  
 sequence  
 <400> 164  
 agcatcgagt cggccttggt g 21

<210> 165  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of the artificial sequence: an artificially synthesized primer  
 sequence  
 <400> 165  
 gcggctgaag acggcctatg t 21

<210> 166  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of the artificial sequence: an artificially synthesized primer  
 sequence  
 <400> 166  
 actttattgt catagtttag atctatttg 30

<210> 167  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of the artificial sequence: an artificially synthesized primer  
 sequence  
 <400> 167  
 ataatcctta aaaactccat ttccaccct 30

<210> 168  
 <211> 1536  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (139).. (1062)  
 <400> 168  
 GTGCTCCGCC GCCCGCCCCG ACCCGGGCCC AGCCGCCTCC ACGGCCCGCG CTCGTACTGG 60  
 AGCGAAGAGC GGCCTCCTGA GGGAGGGGAA GGGACGTGGG GCGGCCACG GCAGGATTAA 120  
 CCTCCATTTC AGCTAATC ATG GGA GAG ATT AAA GTC TCT CCT GAT TAT AAC 171  
 Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn  
 1 5 10



TGG TTT AGA GGT ACA GTT CCC CTT AAA AAG ATT ATT GTG GAT GAT GAT	219
Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp	
15 20 25	
GAC AGT AAG ATA TGG TCG CTC TAT GAC GCG GGC CCC CGA AGT ATC AGG	267
Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg	
30 35 40	
TGT CCT CTC ATA TTC CTG CCC CCT GTC AGT GGA ACT GCA GAT GTC TTT	315
Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe	
45 50 55	
TTC CGG CAG ATT TTG GCT CTG ACT GGA TGG GGT TAC CGG GTT ATC GCT	363
Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala	
60 65 70 75	
TTG CAG TAT CCA GTT TAT TGG GAC CAT CTC GAG TTC TGT GAT GGA TTC	411
Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe	
80 85 90	
AGA AAA CTT TTA GAC CAT TTA CAA TTG GAT AAA GTT CAT CTT TTT GGC	459
Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly	
95 100 105	
GCT TCT TTG GGA GGC TTT TTG GCC CAG AAA TTT GCT GAA TAT ACT CAC	507
Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His	
110 115 120	
AAA TCT CCT AGA GTC CAT TCC CTA ATC CTC TGC AAT TCC TTC AGT GAC	555
Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp	
125 130 135	
ACC TCT ATC TTC AAC CAA ACT TGG ACT GCA AAC AGC TTT TGG CTG ATG	603
Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met	
140 145 150 155	
CCT GCA TTT ATG CTC AAA AAA ATA GTT CTT GGA AAT TTT TCA TCT GGC	651
Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly	
160 165 170	
CCG GTG GAC CCT ATG ATG GCT GAT GCC ATT GAT TTC ATG GTA GAC AGG	699
Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg	
175 180 185	
CTA GAA AGT TTG GGT CAG AGT GAA CTG GCT TCA AGA CTT ACC TTG AAT	747
Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn	
190 195 200	
TGT CAA AAT TCT TAT GTG GTA CCT CAT AAA ATT CGG GAC ATA CCT GTA	795
Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val	
205 210 215	

ACT ATT ATG GAT GTG TTT GAT CAG AGT GCG CTT TCA ACT GAA GCT AAA 843  
 Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys  
 220 225 230 235

GAA GAA ATG TAC AAG CTG TAT CCT AAT GCC CGA AGA GCT CAT CTG AAA 891  
 Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys  
 240 245 250

ACA GGA GGC AAT TTC CCA TAC CTG TGC AGA AGT GCA GAG GTC AAT CTT 939  
 Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu  
 255 260 265

TAT GTA CAG ATA CAT TTG CTG CAA TTC CAT GGA ACC AAA TAC GCG GCC 987  
 Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala  
 270 275 280

ATT GAC CCA TCA ATG GTC AGT GCC GAG GAG CTT GAG GTG CAG AAA GGC 1035  
 Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly  
 285 290 295

AGC CTT GGC ATC AGC CAG GAG GAG CAG TAGTGTGTCT CTCGCTGTCA ATGATGA 1089  
 Ser Leu Gly Ile Ser Gln Glu Glu Gln  
 300 305

GTTGACCCGG TGTGTTCTTG TATAGTCAGT GGCATCAGCA CCCGTCAGCC GGCCTTTTCC 1149  
 TTCAGGTTTCG TCAGGCTCAC CGGTTCTCAC TGTGTCTGGG AAGTAGGACT GATGGTCATC 1209  
 TTCATGACAG GCGGCATCTC CACTAAGCCT GTGTAACGT TCCCTCTTTG GTTTTCTTAG 1269  
 CTTTTGAATT TGAAGAAGTA CTTTGAAGA CTCCCATTTT AAGAACCGTG CAGATTTTGC 1329  
 TACCAAAAGT CTTCAACCACT GTGTTCTTAA GTGAATGTTA ATTTCTGAGG TTTGGGACTT 1389  
 TGTGGTGTTT TTTTCTTCT TTTCTTTTCC ATTCTTCTTT CTTCTTTTT ATGTTGTTTG 1449  
 CTGTAATGTC TGCACATCCA GATTGCATAT CAGGACATTG GTTATTTTAT GCTTTCTTGG 1509  
 ATATAACCAT GATCAGAGTG CCATGGC 1536

<210> 169  
 <211> 308  
 <212> PRT  
 <213> Homo sapiens  
 <400> 169

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr  
 1 5 10 15  
 Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Ser Lys Ile Trp  
 20 25 30  
 Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe  
 35 40 45  
 Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu  
 50 55 60  
 Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val  
 65 70 75 80  
 Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp  
 85 90 95  
 His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly  
 100 105 110  
 Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val

115 120 125  
 His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn  
 130 135 140  
 Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu  
 145 150 155 160  
 Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met  
 165 170 175  
 Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly  
 180 185 190  
 Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn Cys Gln Asn Ser Tyr  
 195 200 205  
 Val Val Pro His Lys Ile Arg Asp Ile Pro Val Thr Ile Met Asp Val  
 210 215 220  
 Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys Glu Glu Met Tyr Lys  
 225 230 235 240  
 Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys Thr Gly Gly Asn Phe  
 245 250 255  
 Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu Tyr Val Gln Ile His  
 260 265 270  
 Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala Ile Asp Pro Ser Met  
 275 280 285  
 Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly Ser Leu Gly Ile Ser  
 290 295 300  
 Gln Glu Glu Gln  
 305

&lt;210&gt; 170

&lt;211&gt; 2560

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

(202).. (1002)

&lt;400&gt; 170

CTGGCCTACT GGGGCTCCAG CCGTGTCTG AGGAGCTGGA CCAGCCACAT CCCCTGGGGC 60  
 TGCAGTTGAA GCAGAACCAA GTGGCCATCC CGGCGTTAGA CCGTAGGTTC CTGGTCCCGG 120  
 AGTGGTCGGA GCGGCCAGT GGGCAGGCAG CTCTTGCTCA CAGGCCGCGG TGCCAGGCC 180  
 GCTGGCTCTC CGCAGGGCGG A ATG GCG CTG CAA GTG GAG CTG GTA CCC ACC 231  
 Met Ala Leu Gln Val Glu Leu Val Pro Thr  
 1 5 10

GGG GAG ATC ATC CGC GTG GTT CAT CCC CAC AGG CCC TGC AAG CTT GCC 279  
 Gly Glu Ile Ile Arg Val Val His Pro His Arg Pro Cys Lys Leu Ala  
 15 20 25

CTG GGC AGT GAC GGG GTT CGG GTG ACC ATG GAG AGT GCG CTC ACC GCC 327  
 Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala Leu Thr Ala  
 30 35 40

CGT GAC CGG GTG GGG GTG CAG GAT TTC GTG CTG CTG GAG AAC TTC ACC 375  
 Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr  
 45 50 55

AGC GAG GCC GCC TTC ATC GGG AAC CTG CGG CGG CGA TTT CGG GAG AAT Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn 60 65 70	423
CTC ATC TAC ACC TAC ATT GGC CCC GTC CTG GTC TCT GTC AAT CCC TAC Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr 75 80 85 90	471
CGG GAC CTG CAG ATC TAC AGC CGG CAG CAT ATG GAG CGT TAC CGT GGC Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly 95 100 105	519
GTC AGC TTC TAT GAA GTG CCC CCT CAC CTG TTT GCC GTG GCG GAC ACT Val Ser Phe Tyr Glu Val Pro Pro His Leu Phe Ala Val Ala Asp Thr 110 115 120	567
GTG TAC CGA GCA CTG CGC ACG GAG CGT CGG GAC CAG GCT GTG ATG ATC Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile 125 130 135	615
TCT GGG GAG AGC GGG GCA GGC AAG ACC GAG GCC ACC AAG AGG CTG CTG Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu 140 145 150	663
CAG TTC TAT GCA GAG ACC TGC CCA GCC CCC GAG CGC GGA GGT GCC GTG Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val 155 160 165 170	711
CGG GAC CGG CTG CTA CAG AGC AAC CCG GTG CTG GAG GCC TTT GGA AAT Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn 175 180 185	759
GCC AAG ACC CTC CGG AAC GAT AAC TCC AGC AGG TTC GGG AAG TAC ATG Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met 190 195 200	807
GAT GTG CAG TTT GAC TTC AAG GGT GCC CCC GTG GGT GGC CAC ATC CTC Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu 205 210 215	855
AGT TAC CCC CTG GAA AAG TCA CGA GTG GTG CAC CAG AAT CAT GGG GAG Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu 220 225 230	903
CGG AAC TTC ACA TCT TCT ACC AGC TGC TGG AGG GGG GCG AGG AGG AGA Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg 235 240 245 250	951
CTC TTC GCA GGC TGG GCT TGG AAC GGA ACC CCC AGA GCT ATC TGT ACC Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr 255 260 265	999
TGG TGAAGCCAG TGTGCCAAAG TCTTCTTCAT CAACGACAAG AGTGACTGGA AGGTGCG	1058

Trp

TCAGGAAGGC TCTGACAGTC ATTGATTTC CCGAGGATGA AGTGGAGGAC CTGCTGAGCA 1118  
 TCGTGGCCAG CGTCCTTCAT TTGGGCAACA TCCACTTTGC TGCCAACGAG GAGAGCAATG 1178  
 CCCAGGTCAC CACCGAGAAC CAGCTCAAGT ATCTGAGCCC ATTCAGTATG CCGTGCCTGT 1238  
 TGTGAAATAC GACCGCAAGG GCTACAAGCC TCGCTCCCGG CAGCTGCTGC TCACGCCCAA 1298  
 CGCCGTCGTC ATCGTGAGG ACGCCAAAGT CAAGCAGAGG ATTGATTACG CCAACCTGAC 1358  
 CGGAATCTCT GTCAGCAGCC TGAGCGACAG TCTTTTTGTG CTTTCATGTAC AGCGTGCGGA 1418  
 CAATAAGCAA AAGGGAGATG TGGTGTGCA GAGTGACCAC GTGATTGAGA CGCTGACCAA 1478  
 GACAGCCCTC AGTGCCAACC GCGTGAACAG CATCAACATC AACCAGGGCA GCATCACGTT 1538  
 TGCAGGGGGC CCCGGCAGGG ATGGCACCAT TGACTTCACA CCCGGCTCGG AGCTGCTCAT 1598  
 CACCAAGGCC AAGAACGGGC ACCTGGCTGT GGTGCCCCA CGGCTGAATT CTCGGTGATA 1658  
 AAGGCGCCCA CTGGACCCTC CCAACGCCCA ATGCTTTGCT TTTCTCCTCC TCCCCTTCCC 1718  
 AGTTACCAAA GACTCGAACT TCCAGACAGG GACCCAGGGA CACCCCGAAG CCCACCTGCA 1778  
 ATCTCCCAAC TCCTGCCCAT CCCTCTCTTG AGGGAGCAGC AGGGGCCAGG AGCTACCCCA 1838  
 GGAGTGGGCC AGGCCGGGCC ACAGCAATAG GAAAGCCAGG GCCAGAGCGA GCCATGCCAG 1898  
 CCCTACTGCC GATGCCAAAT ATTTGAGAGA AGGGAAC TTT TGCTGAGGTT TTCTCTGAGG 1958  
 TTTTTTTTGA TGCTTTATAG GAAACTATTT TTTAAAAAAA GCCATTTCCT ACCCAAGGAC 2018  
 ACAGTGGATG TGTTTTCCCT GACTCCAGCA GGGCAAGGAA ATGTAGCCGA GAGGTTGTGT 2078  
 GGGCTGGGCT CTGGTGCCCT CTTCCCTGGC CAGGACACCT CTCCTCCTGA TTCCCTTGGC 2138  
 ACCTTGCTTT TCTGTCTGTT TACCTGTCTC CCTGCCTGCC CATCTGCATC TTTTGCAGCC 2198  
 CACTCTGACT TCCATCTGGG GGCTGAGACC ACCCTTGCCT GCCCCCTTCT TTCTGCCTTA 2258  
 AGAATGTCCT TTTAGGCTGG GCATGGTGGC TCACGCCTGT AACCCAGCA CTTTGGGAGG 2318  
 CGGAGACGGG CAGATAACCT GAGGTCAGGA TTTTCGAGACC AACCTGACCT ACATGGAGAA 2378  
 ACTCCGCCTC TGGAAGGAT ACAAATTAG CCGGGCATGG TGGTGCACGC CTCTAATCCC 2438  
 AGCTGCTCGG GAGGCTGAGG CAGGAGAATC ACTTGAACCC GGGAAGTGA GGTGACGTG 2498  
 AGCCAAGAGT ACACCACTGC ACTCCAGCCT GGGCAACAGA GCGAGACTCC GTCTTAAAAA 2558  
 AA 2560

&lt;210&gt; 171

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 171

Met Ala Leu Gln Val Glu Leu Val Pro Thr Gly Glu Ile Ile Arg Val  
 1 5 10 15  
 Val His Pro His Arg Pro Cys Lys Leu Ala Leu Gly Ser Asp Gly Val  
 20 25 30  
 Arg Val Thr Met Glu Ser Ala Leu Thr Ala Arg Asp Arg Val Gly Val  
 35 40 45  
 Gln Asp Phe Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile  
 50 55 60  
 Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile  
 65 70 75 80  
 Gly Pro Val Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr  
 85 90 95  
 Ser Arg Gln His Met Glu Arg Tyr Arg Gly Val Ser Phe Tyr Glu Val  
 100 105 110  
 Pro Pro His Leu Phe Ala Val Ala Asp Thr Val Tyr Arg Ala Leu Arg  
 115 120 125  
 Thr Glu Arg Arg Asp Gln Ala Val Met Ile Ser Gly Glu Ser Gly Ala  
 130 135 140  
 Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu Gln Phe Tyr Ala Glu Thr

145		150		155		160									
Cys	Pro	Ala	Pro	Glu	Arg	Gly	Gly	Ala	Val	Arg	Asp	Arg	Leu	Leu	Gln
		165		170		175									
Ser	Asn	Pro	Val	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Leu	Arg	Asn
		180		185		190									
Asp	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Tyr	Met	Asp	Val	Gln	Phe	Asp	Phe
		195		200		205									
Lys	Gly	Ala	Pro	Val	Gly	Gly	His	Ile	Leu	Ser	Tyr	Pro	Leu	Glu	Lys
	210			215		220									
Ser	Arg	Val	Val	His	Gln	Asn	His	Gly	Glu	Arg	Asn	Phe	Thr	Ser	Ser
225				230		235								240	
Thr	Ser	Cys	Trp	Arg	Gly	Ala	Arg	Arg	Arg	Leu	Phe	Ala	Gly	Trp	Ala
				245		250								255	
Trp	Asn	Gly	Thr	Pro	Arg	Ala	Ile	Cys	Thr	Trp					
		260				265									

&lt;210&gt; 172

&lt;211&gt; 2650

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (116).. (1216)

&lt;400&gt; 172

CTTTTGCTGC	TGCGCCCGGG	CAGGGGCTGC	CGCGGCCCCA	GGTCCCGCTT	CGAGACGCGG	60
CGCGGTCCAG	GCGGGAGGCG	ACTCCCTAGG	AAGGGACCCG	GGGCGGGAGG	AGGAA ATG	118
				Met		
				1		

AGG	CCG	CGC	GGA	AGG	AAG	GCG	GCG	AGC	CCC	GGG	GCC	CCG	AGG	CCT	TGG	166
Arg	Pro	Arg	Gly	Arg	Lys	Ala	Ala	Ser	Pro	Gly	Ala	Pro	Arg	Pro	Trp	
		5				10						15				

CCG	CGT	CAC	AGC	ACC	CAC	ATG	GCC	TCT	GGA	GTG	GGC	GCG	GCC	TTC	GAG	214
Pro	Arg	His	Ser	Thr	His	Met	Ala	Ser	Gly	Val	Gly	Ala	Ala	Phe	Glu	
	20					25					30					

GAA	CTG	CCT	CAC	GAC	GGC	ACG	TGT	GAC	GAG	TGC	GAG	CCC	GAC	GAG	GCT	262
Glu	Leu	Pro	His	Asp	Gly	Thr	Cys	Asp	Glu	Cys	Glu	Pro	Asp	Glu	Ala	
	35				40					45						

CCG	GGG	GCC	GAG	GAA	GTG	TGC	CGA	GAA	TGC	GGC	TTC	TGC	TAC	TGC	CGC	310
Pro	Gly	Ala	Glu	Glu	Val	Cys	Arg	Glu	Cys	Gly	Phe	Cys	Tyr	Cys	Arg	
	50				55					60					65	

CGC	CAT	GCC	GAG	GCG	CAC	AGG	CAG	AAG	TTC	CTC	AGT	CAC	CAT	CTG	GCC	358
Arg	His	Ala	Glu	Ala	His	Arg	Gln	Lys	Phe	Leu	Ser	His	His	Leu	Ala	
			70					75						80		

GAA	TAC	GTC	CAC	GGC	TCC	CAG	GCC	TGG	ACC	CCG	CCA	GCT	GAC	GGA	GAG	406
Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly	Glu	
			85					90						95		

GGG GCG GGG AAG GAA GAA GCG GAG GTC AAG GTG GAG CAG GAG AGG GAG Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu 100 105 110	454
ATA GAA AGC GAG GCA GGG GAA GAG AGT GAG TCG GAG GAA GAG AGC GAG Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu 115 120 125	502
TCA GAG GAA GAG AGC GAG ACA GAG GAA GAG AGT GAG GAT GAG AGC GAT Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp 130 135 140 145	550
GAG GAG AGT GAA GAA GAC AGC GAG GAA GAA ATG GAG GAT GAG CAA GAA Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu 150 155 160	598
AGC GAG GCC GAA GAA GAC AAC CAA GAA GAA GGG GAA TCC GAG GCG GAG Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu 165 170 175	646
GGA GAA ACT GAG GCA GAA AGT GAA TTT GAC CCA GAA ATA GAA ATG GAA Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu 180 185 190	694
GCA GAG AGA GTG GCC AAG AGG AAG TGT CCG GAC CAT GGG CTT GAT TTG Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu 195 200 205	742
AGT ACC TAT TGC CAG GAA GAT AGG CAG CTC ATC TGT GTC CTG TGT CCA Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro 210 215 220 225	790
GTC ATT GGG GCT CAC CAG GGC CAC CAA CTC TCC ACC CTA GAC GAA GCC Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala 230 235 240	838
TTT GAA GAA TTA AGA AGC AAA GAC TCA GGT GGA CTG AAG GCC GCT ATG Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met 245 250 255	886
ATC GAA TTG GTG GAA AGG TTG AAG TTC AAG AGC TCA GAC CCT AAA GTA Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val 260 265 270	934
ACT CGG GAC CAA ATG AAG ATG TTT ATA CAG CAG GAA TTT AAG AAA GTT Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val 275 280 285	982
CAG AAA GTG ATT GCT GAT GAG GAG CAG AAG GCC CTT CAT CTA GTG GAC Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp 290 295 300 305	1030
ATC CAA GAG GCA ATG GCC ACA GCT CAT GTG ACT GAG ATA CTG GCA GAC	1078

Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala	Asp	
				310					315					320		
ATC	CAA	TCC	CAC	ATG	GAT	AGG	TTG	ATG	ACT	CAG	ATG	GCC	CAA	GCC	AAG	1126
Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala	Lys	
			325					330					335			
GAA	CAA	CTT	GAT	ACC	TCT	AAT	GAA	TCA	GCT	GAG	CCA	AAG	GCA	GAG	GGC	1174
Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu	Gly	
		340					345					350				
GAT	GAG	GAA	GGA	CCC	AGT	GGT	GCC	AGT	GAA	GAA	GAG	GAC	ACA	TGA	AGGCTT	1225
Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr			
	355					360					365					
GCTACCCCCA	GTGGAAAATC	ATCCCTCCC	CTTGTGTGTA	TGTGACAGCG	TGTATGTAAC											1285
GGCTTCTGAT	TTCTGTGAAA	GCTGCTCAGC	AACAAACGTA	CTTCCACCAG	ATGTGTCCCC											1345
AGATCCACAG	CAGGCACATA	TCTCTCCAAG	GGATGACCAG	TTTTATGCTT	ACTGTGTGCT											1405
TCTCATCCCC	TGGTTGTGGT	AGGTCAAGGA	AAAGAGCCCC	TTTGATCCAC	CAGGAGCAAT											1465
TAAGAAAGGT	CCTTCAGGTA	ATCCCTCAAT	GGCTGCTTTG	AACCTTACTCA	GGAAGCCAG											1525
CCCCCATAAT	ATTGTATTAC	CAAACAGTAT	CGCTTTGTGA	GGAAGGATCT	GGAATAATCT											1585
TGAAGGGAAG	TCAGAGTTTT	CTCCCTGCCT	ATTAACAAAA	ACCCAATTTT	GTTCATATTG											1645
AAGCATGAAA	TAAATGAGAG	CAAGGTAGGG	CCAAATTAAC	TCTTGTGGAC	AGTCCCTAAA											1705
AGTCCAGTTC	TACATTTGTG	AAAATTGTGG	TGCCATGAAT	TAAGATGGAT	GAAGTATCCA											1765
AGGTGTTGGA	GAAAGAGTTA	AAGATGAGGA	AGAGATATTT	TTAGTATATG	AAGTTATCCA											1825
GGACTTGATA	TTCATAATTC	AGTGCTGTGG	AAATGAAAAA	AATGATTGAA	GAGGTGGAAC											1885
GGAAATGACC	TTAGGGGGAA	AAAAAAGGAC	CAAAGAAGTC	TGATTAAAAG	TTGAAATCAG											1945
TATTTCTGAA	TTCAAATTGC	TTGAATTTCC	AAAATAGTCA	GTAAGGATC	TAATAGAACC											2005
AGAATTATTT	GGGTGAATTC	TGCAGGTTTT	ATGGGCTTGT	CACAACGTGA	AGGGCTGGAA											2065
TGTATATTAC	CAAATGGGAA	TTTCCATTGT	AGGTTTTTGC	TAGTCCCACC	CCCATTTTAG											2125
CCTAATTTGG	CTTAAACGCA	GTATGGGGAG	AATTGTTCCC	ATTCCATGTG	TTCTGAATTC											2185
AGCTCATCTC	CCAGCATATA	GATATATCCT	CCTTTAACTC	CGACCAGAAC	CCTTCTTCCT											2245
GTGGCACTCC	CCACCCATAG	ACCTTCAGAT	CATCTCCAC	ACCCTGGATC	TCACTCTCCT											2305
CTTAGTAACA	GAGACACTCC	TGAGGTTGGA	CTTCTTGCT	TTTCTCTACT	TCCAAATCAC											2365
AATTTCTTAC	AACCAAGCTT	TGTGCTCCCG	AGTAAGCAGG	GATGTACTAG	GGGAATGTAA											2425
AACTGCAAAC	TTAAAAACCT	GCATCTTCTT	GAAGCATCAG	TTTACTTAC	CAAATGGTTT											2485
AGAGTCATAA	GATGACCTAT	TTTTATATAA	AAGTTATATT	ATAGAATAAA	ATGTTCATAC											2545
GCATAGACTG	TTAAG															2560

&lt;210&gt; 173

&lt;211&gt; 367

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

173

Met	Arg	Pro	Arg	Gly	Arg	Lys	Ala	Ala	Ser	Pro	Gly	Ala	Pro	Arg	Pro	
1				5					10				15			
Trp	Pro	Arg	His	Ser	Thr	His	Met	Ala	Ser	Gly	Val	Gly	Ala	Ala	Phe	
			20					25					30			
Glu	Glu	Leu	Pro	His	Asp	Gly	Thr	Cys	Asp	Glu	Cys	Glu	Pro	Asp	Glu	
		35				40						45				
Ala	Pro	Gly	Ala	Glu	Glu	Val	Cys	Arg	Glu	Cys	Gly	Phe	Cys	Tyr	Cys	
	50					55					60					
Arg	Arg	His	Ala	Glu	Ala	His	Arg	Gln	Lys	Phe	Leu	Ser	His	His	Leu	



65					70					75				80	
Ala	Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly
				85					90					95	
Glu	Gly	Ala	Gly	Lys	Glu	Glu	Ala	Glu	Val	Lys	Val	Glu	Gln	Glu	Arg
			100					105					110		
Glu	Ile	Glu	Ser	Glu	Ala	Gly	Glu	Glu	Ser	Glu	Ser	Glu	Glu	Glu	Ser
		115					120					125			
Glu	Ser	Glu	Glu	Glu	Ser	Glu	Thr	Glu	Glu	Glu	Ser	Glu	Asp	Glu	Ser
	130					135					140				
Asp	Glu	Glu	Ser	Glu	Glu	Asp	Ser	Glu	Glu	Glu	Met	Glu	Asp	Glu	Gln
145					150					155				160	
Glu	Ser	Glu	Ala	Glu	Glu	Asp	Asn	Gln	Glu	Glu	Gly	Glu	Ser	Glu	Ala
			165					170						175	
Glu	Gly	Glu	Thr	Glu	Ala	Glu	Ser	Glu	Phe	Asp	Pro	Glu	Ile	Glu	Met
			180					185					190		
Glu	Ala	Glu	Arg	Val	Ala	Lys	Arg	Lys	Cys	Pro	Asp	His	Gly	Leu	Asp
		195				200						205			
Leu	Ser	Thr	Tyr	Cys	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys
	210				215					220					
Pro	Val	Ile	Gly	Ala	His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu
225				230					235					240	
Ala	Phe	Glu	Glu	Leu	Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala
			245					250						255	
Met	Ile	Glu	Leu	Val	Glu	Arg	Leu	Lys	Phe	Lys	Ser	Ser	Asp	Pro	Lys
		260					265						270		
Val	Thr	Arg	Asp	Gln	Met	Lys	Met	Phe	Ile	Gln	Gln	Glu	Phe	Lys	Lys
		275				280						285			
Val	Gln	Lys	Val	Ile	Ala	Asp	Glu	Glu	Gln	Lys	Ala	Leu	His	Leu	Val
	290				295						300				
Asp	Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala
305				310						315				320	
Asp	Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala
				325						330				335	
Lys	Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu
			340					345						350	
Gly	Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr	
	355						360						365		

&lt;210&gt; 174

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence:a synthetic DNA

&lt;400&gt; 174

ttaaagcttgc caccatgagc aaccccagcg cccaccacc a

41

&lt;210&gt; 175

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of the artificial sequence:a synthetic DNA

<400> 175

gtatcgattt aattgcgac ccccatcag

29

176

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 176

cacctactglatgacaccacattc

24

<210> 177

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 177

gagatgctgttccatgctggcctg

24

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 178

ggaaagctctccgtggctaacaag

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 179

catagtccttgacaagggtcacag

24

<210> 180

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 180

cccatcaccatcttccaggagc

22

<210> 181

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 181

ttcaccaccttcttgatgtcatcata

26